

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 17:42:00 ; Search time 6486 Seconds
(without alignments)
10932.656 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1636
Sequence: 1 tccgggggtctctccgtccg.....aaaaaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb.ba.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1275	77.9	1275	6	AX040982	AX040982 Sequence
2	707	43.2	1632	8	AK070211	AK070211 Oryza sat
3	702.2	42.9	1611	8	AB024987	AB024987 Oryza sat
4	497.6	30.4	1043	8	OSCYCOS1	X82035 O.sativa mr
5	402.2	24.6	1777	8	AK070518	AK070518 Oryza sat
6	400.6	24.5	1793	8	OSCYCOS2	X82036 O.sativa mr
7	383.4	23.4	1343	8	MSCYCMS2	X69741 M.sativa cy
8	383.4	23.4	1758	8	MVCYCMS2	X82040 M.sativa mr
9	374	22.9	1706	8	MSCYCMS2	X78504 M.sativa mr
10	372.4	22.8	1700	8	MVCYCMS1	X82039 M.sativa mr
11	364.6	22.3	1999	8	LES243455	AJ243455 Lycopersi
12	357	21.8	1255	6	AX449282	AX449282 Sequence
13	357	21.8	1603	8	ZMU10076	U10076 Zea mays B7
14	357	21.8	1715	6	AX449320	AX449320 Sequence
15	356	21.8	1287	6	AX449286	AX449286 Sequence
16	335.2	20.5	1798	8	ATCYC2B	Z31400 A.thaliana
17	335.2	20.5	1725	8	AK107209	Z31401 A.thaliana
18	249.4	15.2	1725	8	AK107209	U66608 Zea mays cy
19	237.6	14.5	1501	8	ZMU66608	Z75660 S.rostrata
20	234.8	14.4	1632	8	SRCYCB1	X62820 G.max mRNA
21	228.2	13.9	1596	8	GMWYC	AF051225 Picea mar
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34	211.4	12.9	1245	8	BT006437	AK111939 Oryza sat
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36	207.8	12.7	1490	8	PUMWICY	D50871 Glycine max
37	206	12.6	1813	8	SOXMCB1TD	U44857 Lupinus lut
38	205.8	12.6	1782	8	LLU44857	U66607 Zea mays cy
39	205	12.5	2190	8	ZMU66607	D50737 Nicotiana t
40	204.8	12.5	1707	8	TOBNTCYCC	Y10161 C.rubrum mr
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ALIGNMENTS

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX040982 1275 bp DNA linear PAT 23-NOV-2000
Sequence 29 from Patent WO0065040.
AX040982
AX040982.1 GI:11340578

Zea mays
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

Helentjaris T.G., Habben J.E. and Sun Y.
Cell cycle genes and methods of use

JOURNAL

Patent: WO 0065040-A 29 02-NOV-2000;
PIONEER HI-BRED INTERNATIONAL, INC. (US)

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Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AK070211

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AK070211 1632 bp mRNA linear. PLN 24-JUN-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J023043123, full
insert sequence.
AK070211 GI:32980235
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

The Rice Full-Length cDNA Consortium, National Institute of
Agricultural Sciences Rice Full-Length cDNA Project Team,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Hotta, I.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuka, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
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Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., FIKEN,
Kawai, J., Carrinci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
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Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Oasato, N., Oca, Y.,
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RESULT 3
 AB024987
 LOCUS
 DEFINITION Oryza sativa cysB2.os.1 mRNA for cyclin, complete cds.
 ACCESSION AB024987
 VERSION AB024987.1 GI:6331703
 KEYWORDS cyclin.
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (sites)
 AUTHORS Umeda,M., Iwamoto,N., Umeda-Hara,C., Yamaguchi,M., Hashimoto,J. and Uchimiya,H.
 TITLE Molecular characterization of mitotic cyclins in rice plants
 JOURNAL Mol. Gen. Genet. 262 (2), 230-238 (1999)
 MEDLINE 99444506
 PUBMED 10517318
 REFERENCE 2 (bases 1 to 1611)
 AUTHORS Umeda,M.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-1999) Masaaki Umeda, University of Tokyo,
 Institute of Molecular and Cellular Biosciences; Yayoi 1-1-1,
 Bunkyo-ku, Tokyo 113-0032, Japan
 (E-mail:mumeda@imcbns.iam.u-tokyo.ac.jp, Tel:81-3-5841-8466,
 Fax:81-3-5841-8466)

FEATURES
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RESULT 4
LOCUS OSCYCOS1 1043 bp mRNA linear PLN 26-NOV-1996
DEFINITION O.sativa mRNA for cyclin 1.
ACCESSION X82035
VERSION X82035.1 GI:558620
KEYWORDS cyclin; cycos1 gene.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 Sauter, M., Mekhedov, S.L. and Kende, H.
Gibberellin promotes histone H1 kinase activity and the expression
of cdc2 and cyclin genes during the induction of rapid growth in
deepwater rice internodes
Plant J. 7 (4), 623-632 (1995)
JOURNAL 95261415
MEDLINE 7742859
PUBMED
REFERENCE 2 (bases 1 to 1043)
AUTHORS Kende, H.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1994) H. Kende, MSU-DOE Plant Research
Laboratory, Michigan State University, East Lansing, MI 48824-1312,
USA

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Query Match 30.4%; Score 497.6; DB 8; Length 1043;
Best Local Similarity 79.0%; Pred. No. 7.2e-110;
Matches 605; Conservative 0; Mismatches 159; Indels 2; Gaps 1;

ORIGIN
659 GCCAACAGACATAACTCAAGATGAGACGAATCTTGATGCTGCTGATGAGGTTTC 718

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Db 1 GTCAAGGAGACATAAAATGAAAAGATGAGAGCAATTCGTATGATTTGGCTCATTTGAGTCC 60
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Db 61 ATCAAAATTTGAGCTGATGATGAGACTCTCTTTCTTATGTTTAAACATAGTAGACAGAT 120
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Db 121 TCTTGGAAAAACAAGTTGTGCCAAGGAAGAGTTGTCAGCTAGTTGGAGTGCACCTATGC 180
QY 839 TGCTCGCTTGTAAATATGAGGAGGTATCTGTTCAGTGTGTTGAGGACCTTTGTGCTGATAT 898
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QY 899 CTGACCGTGCCTACACAAAAGGGCAAAATTTAGAAATGGAAAGTTGATTTCTGACACGC 958
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QY 1019 CAGATGCAGATAAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTGTAG 1078
Db 361 CTCAGTCTGACACAGCAGCTACAGCTACTTCTCTTTTCAFTCTGGAGCTCTCCCTGGTG 420
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RESULT 5
LOCUS AK070518 1777 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023055K12, full
insert sequence.
ACCESSION AK070518
VERSION AK070518.1 GI:32980542
KEYWORDS FLI cDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Teshikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Otsomo, Y., Murakami, K.,

```

Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, H., Kobayashi, M., Xie, Q., Lu, M., Nariawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niihara, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, T., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

Science 301 (5631), 376-379 (2003)

22752273

12869764

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

2 (bases 1 to 1777)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Nami, K., Nariawa, R., Niihara, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Oka, H., Osato, N., Ota, Y., Otonari, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

TITLE

JOURNAL

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@ias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NRAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nami, K., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otonari, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Maeda, H., Miura, J., Mizuno, K., Nariawa, R., Niihara, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

Location/Qualifiers

1..1777

FEATURES

source

/organism="Oryza sativa (japonica cultivar-group)"

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ORIGIN

Query Match 24.6%; Score 402.2; DB 8; Length 1777;

Best Local Similarity 68.6%; Pred. No. 1.3e-86;

Matches 554; Conservative 0; Mismatches 253; Indels 0; Gaps 0;

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DB 604 GATATTGACAGCTGTGATGCAAAATACTCCCTTGCAGTAGTTGAATATGTTGATGAAT 663

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QY 661 CAACAGACATAAATCAAGATGAGACAAATTTGATTTGACTGGCTGATTTGAGGTTTCAAC 720

DB 724 CAAATGACATAAATGAGAGATGCGCGCATTTCTCATCGATTGGCTGATAGAGGTTGCAT 783

QY 721 TACACCTTTTGAATGATGATGAGAGCGCTCTTCTTATGTTAAACATATATAGATAGATTC 780

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QY 1081 TACCAATCTCAATATTCGGCTTTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

DB 1144 TATGAGATGCTCAAAATTCAGCGCTCAATGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1203

QY 1141 TGTGCTATCAATCTGTTGCGACATCGGACAAAGTCTGCGAGTCTCTATAGCAGATACACT 1200

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QY 1261 AGTATGCTG 1320

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DB 1384 TCGGAGCGCGCGTCTCTTCTGCTCAAG 1410

RESULT 6

OSCYCOS2

LOCUS

DEFINITION

ACCESSION

OSCYCOS2 1793 bp mRNA linear PLN 13-FEB-1998

O.sativa mRNA for cyclin 2.

X82036 Y09038

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VERSION X82036.1 GI:1694891
KEYWORDS cyclin; cycOs2 gene.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 1418)
Sauter, M., Mekhedov, S.L. and Kende, H.
Gibberellin promotes histone H1 kinase activity and the expression
of cdc2 and cyclin genes during the induction of rapid growth in
deepwater rice internodes
Plant J. 7 (4), 623-632 (1995)
95261415
7742859
2
Sauter, M.
Isolation and characterization of a cDNA encoding a mitotic cyclin
of the CycB2 type from rice (accession no. X82036)
Unpublished
3
Sauter, M.
Characterization of a full length mitotic cyclin cDNA from Oryza
sativa L
Unpublished
4
Kende, H.
Direct Submission
Submitted (04-OCT-1994) H. Kende, MSU-DOE Plant Research
Laboratory, Michigan State University, East Lansing, MI 48824-1312,
USA
REMARK revised by [3]
REFERENCE 5 (bases 1 to 1793)
AUTHORS Sauter, M.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1996) M. Sauter, Univ. Hamburg, Inst. f.
Allgemeine Botanik, MPII, Ohnhorststrasse 18, D- 22609 Hamburg,
FRG
COMMENT On Nov 28, 1996 this sequence version replaced gi:558622.
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Query Match 24.5%; Score 400.6; DB 8; Length 1793;
Best Local Similarity 68.5%; Pred. No. 3.1e-86;
Matches 553; Conservative 0; Mismatches 254; Indels 0; Gaps 0;
ORIGIN
MSCYCMS2
LOCUS M.sativa CYCMS2 mRNA for cyclin. 1343 bp linear PLN 30-JUN-1993
DEFINITION X68741 S53352
ACCESSION X68741.1 GI:19598
VERSION cyclin; cyclin homolog.
KEYWORDS Medicago sativa
SOURCE Medicago sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.
1
Hirt, H., Mink, M., Pfosser, M., Bogre, L., Gyorgyey, J., Jonak, C.,
Gartner, A., Dudits, D. and Heberle-Bors, E.
REFERENCE
AUTHORS

```

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541 GATATTGACAGTGCAGACTCGGGGAACCCGCTTCTGCAACAGATATGTTAAGACTT 600
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RESULT 7
MSCYCMS2

TITLE Alfalfa cyclins: differential expression during the cell cycle and in plant organs
JOURNAL Plant Cell 4 (12), 1531-1538 (1992)
MEDLINE 93104677
PUBMED 1307238
REFERENCE 2 (bases 1 to 1343)
AUTHORS Hirt,H.
TITLE Direct Submission
SUBMITTED (14-OCT-1992) H. Hirt, Inst of Microbiology, Univ of Vienna, Biocenter, Dr Bohrgasse 9, 1030 Vienna, AUSTRIA
FEATURES
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RESULT 8
MVCYCM2 1758 bp mRNA linear PLN 19-JUL-1995
LOCUS M.varia mRNA for mitotic cyclin 2.
DEFINITION X82040
ACCESSION X82040.1 GI:914862
VERSION X82040.1
KEYWORDS cyclin 2 gene.
SOURCE Medicago sativa subsp. x varia
ORGANISM Medicago sativa subsp. x varia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotids;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 1758)
AUTHORS Meskine,I., Bogre,L., Dahl,M., Pirck,M., Ha,D.T., Swoboda,I.,
Heberle-Bors,E., Ammerer,G. and Hirt,H.
TITLE cyclin3, a novel B-type alfalfa cyclin gene, is induced in the
G0-to-G1 transition of the cell cycle
JOURNAL Plant Cell 7 (6), 759-771 (1995)
MEDLINE 95375541
PUBMED 7647566
REFERENCE 2 (bases 1 to 1758)
AUTHORS Pirck,M.
TITLE Direct Submission
SUBMITTED (04-OCT-1994) M. Pirck, Inst for Microbiology & Genetics,
University of Vienna, Dr. Bohrg. 9, 1030 Vienna, AUSTRIA
COMMENT Related sequences: X88740, X88741, S53351 and S53352.
FEATURES
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RESULT 10

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MVCYCMS1
LOCUS      MVCYCMS1
DEFINITION M.varia mRNA for mitotic cyclin 1.
ACCESSION X82039
VERSION    X82039.1 GI:914860
KEYWORDS   cyclin gene.
SOURCE     Medicago sativa subsp. x varia
ORGANISM   Medicago sativa subsp. x varia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Medicago.
REFERENCE  1
AUTHORS    Meskane, I., Bogue, L., Dahl, M., Pirck, M., Ha, D.T., Swoboda, I.,
            Heberle-Bors, E., Amerer, G. and Hirt, H.
TITLE      Cym3, a novel S-type alfalfa cyclin gene, is induced in the
            G0-to-G1 transition of the cell cycle
JOURNAL    Plant Cell 7 (6), 759-771 (1995)
MEDLINE    95375541
PUBMED     7647566
REFERENCE  2 (bases 1 to 1700)
AUTHORS    Pirck, M.
TITLE      Direct Submission
JOURNAL    Submitted (04-OCT-1994) M. Pirck, Inst for Microbiology & Genetics,
            University of Vienna, Dr. Bohrg. 9, 1030 Vienna, AUSTRIA
COMMENT    Related sequences: X68740, X68741, S53351 and S53352.
            Location/Qualifiers
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FEATURES   source

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Best Local Similarity 65.8%; Pred. No. 2.2e-79;
Matches 541; Conservative 0; Mismatches 281; Indels 0; Gaps 0;

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QY      586 TATGTTAAAGAGCTTTACACCTTTTACAGAGAAAATGAGGCTTAAGAGTTGTCTAAGGCCA 645
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QY      646 GATTACATGTCACGCAACAGAGACATAAACTCAAGATGAGAGCAATCTGTATTCAGTGG 705
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QY      706 CTGATTGAGTTCACTACAAAGTTTGAACCTGATGATGAGAGGATATCTTTCCAGTTGTTGAGGAC 765
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QY      766 ATAATAGATAGATTCTTGGAAAAGGAGTGTTCAGAGGAAGAGCTCAACTGTTGCTGGA 825
Db      826 CTTATAGACAGATTTTGGAAAAGCAGTCTGTGTTTGAAGAGCTTCAGTTGTTGTTGTT 885
QY      826 GTCACAGCTATGCTGCTGCTGCTGTTGTAATATGAGAGGATATCTTTCCAGTTGTTGAGGAC 885
Db      886 TTAGTGGCAATGCTTTTGGCATGCAAGTATGAGGAAGTTTCAGTGCCTGTGTTGAGAT 945
QY      886 CTTGTGCTGATATCTGACCGTGCTTACACAAAAGGGCAAAATTTTGAAGATGGAAGATTG 945
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RESULT 11

LES243455 1999 bp mRNA linear PLN 29-AUG-2000
 LOCUS Lycopersicon esculentum mRNA for cyclin B2 (CycB2 gene).
 DEFINITION AJ243455

VERSION AJ243455.1 GI:5420281
 KEYWORDS cycB2 gene; cyclin B2.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum

REFERENCE 1
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 JOURNAL asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 2
 AUTHORS Joubes, J., Walsh, D., Raymond, P. and Chevalier, C.
 TITLE Molecular characterization of the expression of distinct classes of
 JOURNAL cyclins during the early development of tomato fruit
 MEDLINE Planta 211 (3), 430-439 (2000)
 PUBMED 20441870

REFERENCE 3
 AUTHORS Chevalier, C.
 TITLE Direct Submission
 JOURNAL Submitted (01-JUL-1999) Chevalier C., Unite de Physiologie
 Vegetale, Institut National de la Recherche Agronomique, B.P. 81,
 33893 Villenave d'Ornon cedex, FRANCE

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Query Match 22.3%; Score 364.6; DB 8; Length 1999;
 Best Local Similarity 60.9%; Pred. No. 1.8e-77;
 Matches 613; Conservative 0; Mismatches 389; Indels 5; Gaps 1;

QY 526 GATGAATTGCTATGATATTCACAGTGCAGACTCGGGAACCGCTGCTGCAACAGAA 585
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QY 586 TATGTTAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTTAAGAGTTGTGAAGCCA 645
 Db 922 TATGTGGAGATTTGTTGCTTAACATCAGAACAAATGAGAGTTAATAGCTGTCTTCCA 981
 QY 646 GATTACATGTCACAGCAACAAGACATAAATCAAGATGAGAGCAATTTCTGATGACTGG 705
 Db 982 TACTATATGGCAACAAGAGCTGACATCAATGAGAGAATCGCGTCTATCTTGATTGACTGG 1041
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RESULT 12

AX449282
 LOCUS AX449282 1255 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 1 from Patent WO0185946.
 ACCESSION AX449282
 VERSION AX449282.1 GI:21698029
 KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE Inze, D., Boudolf, V., de Veylder, L., Acosta, J. A., and Magyar, Z.
AUTHORS Nucleic acid molecules encoding plant cell cycle proteins and uses
TITLE therefor
JOURNAL Patent: WO 0185946-A 1 15-NOV-2001;
CropDesign N.V. (BE)
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Best Local Similarity 63.7%; Pred. No. 1.2e-75;
Matches 543; Conservative 0; Mismatches 310; Indels 0; Gaps 0;
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Db 172 GAGATTGAAATGGAAGATGACAGACAAAGAGAGAGCCCTGTGATGATTTGATCCCTGT 231
QY 556 GACTCGGGGACCCGCTTGTGCAACAGAGATATGTTAAAGAGCTTTACACCTTTTACAGA 615
Db 232 GATAGAAATATCTTTGGCTGGGTGAATATATCATGATGATGATGATGATGATGATGATGAT 291
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Db 292 AATTTTGAAGAACTTAGTTGCGTGCCTCTAATATGATGATGATGATGATGATGATGATGAT 351
QY 676 TCAAGATGAGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
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Db 412 ATGAGAGAACTCTTATCTCACATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471
QY 796 GTTCCAGGAGAGAGCTACAACTGTTGAGTGCAGCTATGATGATGATGATGATGATGATGATGAT 855
Db 472 ATCGTGAGGAGAAAGCTTCAGCTGTGTTGGTGTACTGCTTTGTTGCTGATGATGATGATGATGAT 531
QY 856 GAGAGGATCTGTGTCAGTGTGTTGAGAGCTTGTGCTGATATCTGACCGTGCCTACACA 915
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QY 976 GTTCCACACCTTATGCTTCATGAGAGGTTTCTGAAAGCTGCAGATGATGATGATGATGATGATGAT 1035
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QY 1336 TTCCTGCTGGAGT 1348
Db 1012 TTCTGATTAAT 1024

RESULT 13
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LOCUS Zea mays B73 cyclin III2m mRNA, complete cds. PLN 27-JUL-1994
DEFINITION Zea mays B73 cyclin III2m mRNA, complete cds.
ACCESSION U10076
VERSION U10076.1 GI:516547
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1603)
Renudin, J. P., Colasanti, J., Rime, H., Yuan, Z. and Sundaresan, V.
Cloning of four cyclins from maize indicates that higher plants
have three structurally distinct groups of mitotic cyclins
Proc. Natl. Acad. Sci. U.S.A. 91 (15), 7375-7379 (1994)
94316698
8041798
2 (bases 1 to 1603)
Sundaresan, V.
Direct Submission
Submitted (25-MAY-1994) Venkatesan Sundaresan, Cold Spring Harbor
Laboratory, P.O. Box 100, 1 Bungtown Road, Cold Spring Harbor, NY
11724, USA

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ORIGIN
Query Match 21.8%; Score 357; DB 8; Length 1603;
Best Local Similarity 64.9%; Pred. No. 1.2e-75;
Matches 528; Conservative 0; Mismatches 285; Indels 0; Gaps 0;
QY 541 GATATTGACAGTGCAGACTCGGGAACCCGCTTGTGCTGCAACAGAAATATGTTAAAGAGTT 600
Db 479 GATATTGACAGTGTGATGACAGAAATTTCTCTGCTGTGGCTGACTAGTATGATGAAAT 538
QY 601 TACACCTTTACAGAGAAATGAGCTAAGAGTTGTGTAGGCCAGATATCATCTCCAGC 660
Db 539 TACAGATTTTACAGAAACTGAGGCTGCAAGCTCGCTCCCTCAAAATTTATGTCAAGC 598
QY 661 CAACAGACATAAACTCAAGATGAGAGCAATTTCTGATTGACTGGCTGATTGAGTTTCA 720

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659 TACAACATGAGCTGTTGGAGGAGACCCCTTTTCTAACCCGTGAACATCATAGACAGATTC 718
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841 CTCCTGTTGAATATGAGGAGTATCTGTTCCAGTCTGTTGAGGACCTTGTGCTGATATCT 900
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901 GACCGTGCCTACACAAAAGGCAAAATTTAGAAATGAAAAAGTTGATTTCTGAACACGCTG 960
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1021 GATCAGATAAACAGCTTGAGTACGCTCAATTTTTTCATGCTGGAGCTCTGCTTGGTAGAA 1080
959 CAATCAGAGAAGAGCTCGAACTCCTGCTTTTCTCATGATCGAGTTGAGTCTGTGCAA 1018
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RESULT 14
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DEFINITION Sequence 39 from Patent WO0185946.
ACCESSION AX449320
VERSION AX449320.1 GI:21698067
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
Nucleic acid molecules encoding plant cell cycle proteins and uses
thereof.
Patent: WO 0185946-A 39 15-NOV-2001;
CropDesign N.V. (BE)
Location/Qualifiers
1..1715
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
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AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

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Query Match 21.8%; Score 357; DB 6; Length 1715;
Best Local Similarity 63.7%; Pred. No. 1.2e-75;
Matches 543; Conservative 0; Mismatches 310; Indels 0; Gaps 0;
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RESULT 15
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DEFINITION Sequence 5 from Patent WO0185946.
ACCESSION AX449286
VERSION AX449286.1 GI:21698033
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE

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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
Inze, D., Boudolf, V., de Veylder, L., Acosta, J. A. and Magyar, Z.
Nucleic acid molecules encoding plant cell cycle proteins and uses
therefor
JOURNAL Patent: WO 0185946-A 5 15-NOV-2001;
CropDesign N.V. (BE)
FEATURES
Location/Qualifiers
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/organism="Arabidopsis thaliana"
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ORIGIN
Query Match 21.8%; Score 356; DB 6; Length 1287;
Best Local Similarity 63.9%; Pred. No. 2e-75;
Matches 539; Conservative 0; Mismatches 305; Indels 0; Gaps 0;
QY 501 AGAGAACAGGACATTATGAACGAGATGAATGCTCATGGATATTGACAGTGCAGACTC 560
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Db 1266 AGTG 1269

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Job time : 6491 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 15:08:29 ; Search time 674 Seconds
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Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

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Listing first 45 summaries

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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	356	21.8	1287	6 AAS96276	Aas96276 Arabidops
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6	223.4	13.7	274	7 ABX81803	Abx81803 Corn ear-
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9	191.8	11.7	1385	3 AAC42253	Aac42253 Arabidops
10	161.4	9.9	1553	3 AAC77911	Aac77911 Human can
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14	158.6	9.7	1401	3 ABK12023	Abk12023 Human cyc
15	155.6	9.5	2308	6 AB199379	Ab199379 Mouse isc
16	155.4	9.5	1452	2 AAQ37741	Aaq37741 Complete
17	155.4	9.5	1452	2 AAV30100	Aav30100 Complete
18	155.4	9.5	1452	6 AAV62877	Aav62877 Breast ca
19	155.4	9.5	1452	6 AB167953	Ab167953 Ovary can
20	155.4	9.5	1452	6 AB165385	Ab165385 Lung can
21	155.4	9.5	1452	6 AB162871	Ab162871 Colon ade
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28	155.4	9.5	7477	7 ACC44992	Acc44992 Vector pc
29	155.4	9.5	7477	8 ADB85371	Adb85371 Vector DN
30	153.8	9.4	1302	2 AAT41775	Aat41775 Human cyc
31	152	9.3	1278	7 ABT18843	Abt18843 Aspergill
32	152	9.3	1347	7 ABT18249	Abt18249 Aspergill
33	152	9.3	1464	7 ABT20663	Abt20663 Aspergill
34	152	9.3	1577	7 ABT20065	Abt20065 Aspergill
35	152	9.3	3347	7 ABT17655	Abt17655 Aspergill
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38	128.4	7.8	625	9 ADD17214	Add17214 DNA (Seq)
39	125.6	7.7	1646	2 AAQ13385	Aaq13385 Human cyc
40	125.6	7.7	1649	2 AAV16888	Aav16888 Human pro
41	125.6	7.7	1649	2 AAX28023	Aax28023 Prostate
42	125.6	7.7	1649	3 AAZ87508	Aaz87508 Cyclin A
43	125.6	7.7	1649	4 AAS03727	Aas03727 Biomarker
44	125.6	7.7	1649	6 ABL69120	Abi69120 Kidney ca
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ALIGNMENTS

RESULT 1
AAC83108
ID AAC83108 standard; DNA; 1275 BP.
XX
AC AAC83108;
XX
DT 23-FEB-2001 (first entry)
XX
DE DNA encoding a protein involved in the cell cycle SEQ ID 29.
XX
KW Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
KW cotton; rice; barley; millet; ds.
XX
OS Zea mays.
XX
PN WO200065040-A2.
XX
PD 02-NOV-2000.
XX
PF 13-APR-2000; 2000WO-US009975.
XX
PR 22-APR-1999; 99US-0130849P.
XX
PI (PION-) PIONEER HI-BRED INT INC.
XX
PI Helentjaris TG, Habben JE, Sun Y;
XX
DR WPI; 2000-687333/67.
XX
DR P-PSDB; AAB35801.
XX
PT Nucleic acids useful for producing transgenic plants, preferably maize,
PT with increased cell cycle gene activity, preferably activity of cyclin
PT and/or cyclin-dependent kinase.
XX
PS Claim 1; Page 104-106; 122pp; English.
XX
CC Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
CC AAB35806 which are involved in regulating the cell cycle. The protein and
CC DNA sequences have been isolated from Zea mays (corn), and the invention
CC also includes oligonucleotides AAC83114 - AAC83139 which are related to
CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
CC are useful for producing transgenic plants such as maize, soybean,
CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
CC millet with increased levels of cell cycle gene activity, such as
CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are

XX The invention relates to a novel cell cycle protein (CCP) and the
CC polynucleotides encoding them. CCP is useful for identifying a compound
CC which modulates the activity of the polypeptide and which binds to the
CC polypeptide and an anti-CCP antibody is useful for detecting the presence
CC of CCP in a sample. A CCP modulator is useful for modulating the cell
CC cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat,
CC maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP
CC nucleic acid and polypeptide molecules are useful as modulating agents in
CC regulating cell cycle progression in plants. CCP is useful to treat
CC disorders characterised by insufficient or excessive production of CCP
CC protein or production of CCP protein forms which have decreased or
CC aberrant activity. Compounds that bind to or modulate the activity of CCP
CC polypeptide are useful as herbicides or plant growth regulators. The
CC polynucleotide is useful for modifying cell fate, plant development,
CC plant morphology, biochemistry and/or physiology, the length of the G1,
CC S, G2 and/or M phases of the cell cycle of a plant, initiation, promotion,
CC stimulation or enhancement of cell division, DNA replication, seed set,
CC seed size, seed development, tuber, fruit, leaf formation, shoot and root
CC initiation and/or development, nodule function, dwarfism in plants,
CC senescence, tolerance or resistance to stress. CCP, the polynucleotide
CC and the anti-CCP antibody are useful in agriculture to modulate the
CC protein levels or activity of a protein involved in the cell cycle due to
CC environmental conditions, including abiotic stress such as cold, nutrient
CC deprivation, heat, drought, salt stress, or biotic stress such as
CC pathogen attack, to modulate e.g. enhance crop yields, and attenuate
CC plant architecture, plant quality traits, plant reproduction and seed
CC development, endoreduplication in storage cells, storage tissues and/or
CC storage organs of plants or its parts. CCP is useful as an immunogen to
CC generate antibodies. CCP protein is useful to screen for naturally
CC occurring CCP substrates. The polynucleotide is useful for expressing CCP
CC protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to
CC modulate CCP activity. The present sequence encodes a CCP protein of the
CC invention

XX
SQ Sequence 1255 BP; 427 A; 214 C; 274 G; 340 T; 0 U; 0 Other;

Query Match 21.8%; Score 357; DB 6; Length 1255;

Best Local Similarity 63.7%; Pred. No. 4.9e-84;

* Matches 543; Conservative 0; Mismatches 310; Indels 0; Gaps 0;

QY 496 GCGACAGACAGGACATTTATCAAGAGATGTAATGCTCATGGATATTGACAGTGCA 555
DB 172 GAGATTGAATGGAGATGCGACACAAAGAGAGAGCGCTGTGATCGATATTGCTGT 231
QY 556 GACTCGGGGAAACCGCTTGCTGCGACAGAAATATGTTAAAGAGCTTTACACCTTTTACAGA 615
DB 232 GATAAGAATAATCCTTTGGCTGCGGTGAATATATCCATGATATGCAATACCTTCTACAAG 291
QY 616 GAAATGAGGCTAAGAGTTGTTAAGCCAGATTACATGTCCAGCCCAACAGACATAAAC 675
DB 292 AATTTTGAGAAACTTAGTTGGTGGCTCCCTTACTATATGACATCAACAGATCTTAAT 351
QY 676 TCAAGATGAGAGCAATTTCTGATGCTGGCTGATGAGTTCACTACAAAGTTGAACTG 735
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QY 796 GTTCCAGAGGAAGAGCTACAACTGGTTGAGTCCAGCTATGCTGCTGCTGTTGAAATAT 855
DB 472 ATCGTGAGGAAAGAGCTTCACTGTTGTTGTTACTGCTTGTGCTGATGTAATAT 531
QY 856 GAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACA 915
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DB 652 CTACCACTCATATGTTTTCATGAACGATTTCTCAAAGCTGCCCAATCTGCAAGAG 711
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QY 1156 TGCCAGCACTCGCAAAAGGCTTCGAGTCTCATAGCAGATACACTAGCGCAACTCTCTG 1215
DB 832 TTTGAAGAATGGAGCAAAACCTGTGAGTTTTCACACAGGCTACAAAGAAAACAGCTACTG 891
QY 1216 GAGTCTCGAGGATGATGTTAGATTTTTCACAGAGGCTGGAACCACTTAAGCTCACTGGC 1275
DB 892 GCATGTGCGAAGAGATGTTGCTTTTCATCAAGGCGAGGACAGGAGAGCTCACAGGA 951
QY 1276 GTGCACAGAGAGTACAGTACCTACAGTTGCTGCTGCGCAAGATTTTTCCTGCGGAG 1335
DB 952 GTTCACAGAAAGTACACACATCTAAGTTCTGTCTCATGCTGCAGAGACTGAACACAGCTGGG 1011
QY 1336 TTCTGCTGGAGT 1348
DB 1012 TTTCTGATTAAT 1024

RESULT 3

AAS96310

ID AAS96310 standard; cDNA; 1715 BP.

XX AAS96310;

XX 26-FEB-2002 (first entry)

XX Arabidopsis cDNA encoding cell cycle protein CCP1.

XX Cell cycle protein; CCP; ss; cell cycle regulation; herbicide;

KW plant growth regulator; plant development; abiotic stress; biotic stress;

KW nutrient deprivation; pathogen attack; crop yield.

XX Arabidopsis thaliana.

XX WO200185946-A2.

XX 15-NOV-2001.

XX 14-MAY-2001; 2001WO-IB001307.

XX 12-MAY-2000; 2000US-0204045P.

XX (CROP-) CROPDESIGN NV.

XX Inze D, Boudolf V, De Veylder L, Acosta JAT, Magyar Z;

XX WPI; 2002-062249/08.

XX P-PSDB; AAU72520.

XX New cell cycle protein and nucleic acid molecule encoding it useful for

PT regulating cell cycle progression in plants and for identifying

PT modulators which are useful as herbicides or plant growth regulators.

XX Claim 38; Fig 1; 316pp; English.

XX The invention relates to a novel cell cycle protein (CCP) and the

CC polynucleotides encoding them. CCP is useful for identifying a compound

CC which modulates the activity of the polypeptide and which binds to the

CC polypeptide and an anti-CCP antibody is useful for detecting the presence

CC of CCP in a sample. A CCP modulator is useful for modulating the cell

CC cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat,

CC maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP

CC S. G2 and/or M phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, seed size, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, module function, dwarfism in plants, senescence, tolerance or resistance to stress. CCP, the polynucleotide and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to environmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or biotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to generate antibodies. CCP protein is useful to screen for naturally occurring CCP substrates. The polynucleotide is useful for expressing CCP protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence encodes a CCP protein of the invention

XX
SQ Sequence 1287 BP; 404 A; 223 C; 313 G; 347 T; 0 U; 0 Other;

Query Match 21.8%; Score 356; DB 6; Length 1287;
Best Local Similarity 63.9%; Pred. No. 9.2e-84;
Matches 539; Conservative 0; Mismatches 305; Indels 0; Gaps 0;

QY 501 AGAGAACAGGACATATGAAACGAGATGATTTGCTCATGATATGACAGTGCAGACTC 560
Db 426 AGTTGAGATGGAGATGTAACAGTGGAGAACCGATCGTGGATATCGATGCTCTAGACTC 485

QY 561 GGAGAACCCCTGCTCAACAGATATGTTAAAGAGCTTTACACCTTTTACAGAAAA 620
Db 486 GAGAACTCCCTGCGCTGTTGAAATGTTCAAGATCTTTAGCGATTTTACAGACAT 545

QY 621 TGAGGCTAAGAGTTGTGTAAGGCGAGATATCATGTCCAGCCCAACAGACATAAATCAA 680
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Db 606 GATGAGAGCAATCTGATTCAGTGGCTGATGAGTTCACTACAAGTTTGAACCTGATGA 665

QY 741 TGAGACGCTCTTTCTTATGTTAAACATATAGATAGATTTCTGAAAGAAAGTGTTC 800
Db 666 CGAGACACTGTTCTGACAGTGAATCTGATAGATAGATTTCTGCAAGCAAAATGTTAT 725

QY 801 AAGGAGAGCAATCTGATTCAGTGGCTGATGAGTTCACTACAAGTTTGAACCTGATGA 860
Db 726 GAGAAAGAGCTTCCAGCTTGTAGGTTAGTACCTTGTGCTGTTAGTATGATGATGAGGA 785

QY 861 GGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTTACAAAAAGG 920
Db 786 GGTTCGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 845

QY 921 GCAATTTTGAATAGGAAAGTTGATTTGAAACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 980
Db 846 CGATGTTCTAGAGATGGAGAAAACATGTTGAGTACTTTGCAATTTCAATATCTCGTACC 905

QY 981 AACACCTTATGTTCTATGAGAGGTTTCTGAAAGCTGCAATGCAATGCAATGCAATGCA 1040
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QY 1341 GCTG 1344
Db 1266 AGTG 1269

RESULT 5
ADD15948
ID ADD15948 standard; CDNA; 627 BP.
XX
AC ADD15948;
XX
DT 15-JAN-2004 (first entry)
XX
CDNA (seqID 16) that confers an altered visual phenotype in plants.
XX ss: visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; wet leaf; stunting; elongation; texture;
XX agronomic trait; growth regulation; dwarf variety; insect resistance; heat stress; transgenic.
XX Nicotiana benthamiana.
XX WO2003020741-A1.
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027880.
XX
XX 31-AUG-2001; 2001US-0316326P.
XX
XX (DOWC) DOW CHEM CO.
XX (DOWC) DOW AGROSCIENCES LLC.
XX
XX Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;
XX WPI; 2003-300858/29.
XX
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for conferring altered visual phenotypes in plants.
XX
XX Claim 1; SEQ ID NO 16; 517pp; English.
XX
XX This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the polynucleotides described herein. This polynucleotide sequence is a contig cDNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.

XX
SQ Sequence 627 BP; 182 A; 116 C; 140 G; 199 T; 0 U; 0 Other;

Query Match 18.4%; Score 301.2; DB 9; Length 627;
Best Local Similarity 68.0%; Pred. No. 2.2e-69;
Matches 420; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 789.
 DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 KW Arabidopsis thaliana.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX WO200216555-A2.
 PN 28-FEB-2002.
 PD 24-AUG-2001; 2001WO-US026685.
 XX 24-AUG-2000; 2000US-0227866P.
 XX 26-JAN-2001; 2001US-024647P.
 PR 22-JUN-2001; 2001US-030011P.
 XX (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Harper JP, Kreps J, Wang X, Zhu T;
 PI WPI; 2002-304127/34.
 DR Identifying a stress condition to which a plant cell has been exposed and
 XX producing plants with increased tolerance to these abiotic stresses.
 PT Claim 144; SEQ ID NO 789; 577bp + Sequence Listing; English.
 PS The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 1338 BP; 381 A; 281 C; 329 G; 347 T; 0 U; 0 Other;
 Query March 13.1%; Score 214.6; DB 6; Length 1338;
 Best Local Similarity 54.5%; Pred. No. 3.1e-46;
 Matches 452; Conservative 0; Mismatches 374; Indels 3; Gaps 1;
 QY 516 TATGAACGAAGATGAATTCCTCATCGATATTGACAGTCGACGTCGGGGAAACCGCTTGC 575
 DB 474 TATAGTCAACAACCAAGATTATCGATATTGATGATCTGACAAAGATAACCAATTGGC 533
 QY 576 TGCACAGAAATATGTTAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTG 635
 DB 534 TGCCTGGAGTATGTTGATGATATGCTCTCTCTATTAAGAGTTGAGAGGAGTCA 593
 QY 636 TGTAAAGCCAGATTACATGTCGAGCCACCAAGACATAAATCAAGATGAGAGCAATTC 695
 DB 594 GCCTAAGATG---TACATGCACATTCAGACTGAATGATGAGAGATGAGAGGCACTT 650
 QY 696 GATTGACTGGCTGATGAGGTTCTACTACAAGTTTGAACCTGATGATGAGAGCTCTTTCT 755
 DB 651 GATTGATGGTTACTAGAAGTTTCATCAAGTTTGAGCTCAACCTTGAAACTCTGTACCT 710
 QY 756 TATGTTAAACATAATAGATAGATCTCTTGGAAAGAGAGTGTCTCAAGGAGAGACTACA 815
 DB 711 CACCGTCAACATCATGATGATCTCTCTCTGTAAGCTGTCTCTAAAGAGAGTTACA 770
 QY 816 ACTGTTGAGTCAAGATATGCTGCTCTCTGTTGTAATATATGAGAGGATCTGTTCCAGT 875
 DB 771 GCTAGTGGAAATCAGTGCTCTGCTTATGCTTCCAAATATGAAGAAATCTGCCACCTCA 830
 QY 876 TGTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACAAAGGCCAAATTTTAGAAT 935

DB 831 GGTAAACGATCTGGTGTATGTCA CGGAATGCTTACAGTAGCAGACAGATTCGGTAT 890
 QY 936 GGAAAAGTTGATTCGAAACACGCTGCACTTCAACATGCTCTGTTTCAACACCTTATGCTTT 995
 DB 891 GGAGAAGGCAATTTCTTGGAAAACCTCGAATGGTATTTTGACAGTCCCGACTCAATACGCTTT 950
 QY 996 CATGAAGAGGTTTCTGAAAAGCTGCGAGATGCGAGATAAACAAGCTTGAGCTAGCGTCAATTTT 1055
 DB 951 CTTTTCGCTTCATCAAAAGCTTCGATGCTGTGATCCAGAAATGAGATAATGGTTCATT 1010
 QY 1056 CATGCTGAGCTCTGCTTTGGTAGAATACCAATGCTGAATTAATCGGCTTCGCACTCTGGC 1115
 DB 1011 CTTTCTGAAATTTGGGGATGATGATACGACACCTTGACGTTCTGTCTCCCTCCATGCTTGC 1070
 QY 1116 TGCTGCTGGGTTTATACTGACAGTGTGCTATCAATGTTGCCAGCAGCTGCAAAAGGT 1175
 DB 1071 TGCTTCAGCTGTTTACACGGCAAGATGCTCATTTGAACAGTCCCTCTGTTGACTGATAC 1130
 QY 1176 CTGCGAGTCTCATAGCAGATACACTAGCGCAACTCTCTGAGTGTCTCGAGGATGATGGT 1235
 DB 1131 ATTGCAGTTCCACACCGGCTACACAGAGTCTGAGATTATGAGCTGCTCAAGCTTTTAGC 1190
 QY 1236 AGATTTTCCACAGAGGCTGGNACGAGTAAGCTCACTGGCTGCGAGAGAGTACAGTAC 1295
 DB 1191 TTTTCTTCACTGCGAGATCGGTTGAGAGCAGGCTAGCTGAGTGTACAAGAAGTACTCGAA 1250
 QY 1296 CTCAAAGTTCCGTTCCGTCGCGCAAGATTTTGCCTGCGCAGTTCCTCTG 1344
 DB 1251 GGCAGAGATGAGGTTGTTGTTATGTTTCTCGGCCAAGTCTCTCTTG 1299
 RESULT 8
 AAC83106
 ID AAC83106 standard; DNA; 1980 BP.
 XX AAC83106;
 AC AAC83106;
 XX 23-FEB-2001 (first entry)
 DT DNA encoding a protein involved in the cell cycle SEQ ID 21.
 DE Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
 KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
 KW cotton; rice; barley; millet; ds.
 XX Zea mays.
 XX WO200065040-A2.
 XX 02-NOV-2000.
 XX 13-APR-2000; 2000WO-US009975.
 XX 22-APR-1999; 99US-0130849P.
 XX (PION-) PIONEER HI-BRED INT INC.
 XX Helentjaris TG, Habben JE, Sun Y;
 XX WPI; 2000-587333/67.
 DR P-PSDB; AAB35799.
 XX Nucleic acids useful for producing transgenic plants, preferably maize,
 PT with increased cell cycle gene activity, preferably activity of cyclin
 PT and/or cyclin-dependent kinase.
 XX Claim 1; Page 97-99; 122pp; English.
 CC Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
 CC AAB35806 which are involved in regulating the cell cycle. The protein and
 CC DNA sequences have been isolated from Zea mays (corn), and the invention
 CC also includes oligonucleotides AAC83114 - AAC83139 which are related to

the cell cycle polynucleotides. The cell cycle polynucleotide sequences are useful for producing transgenic plants such as maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet with increased levels of cell cycle gene activity, such as activity of cyclin and cyclin-dependent kinases. The DNA sequences are also useful as probes for detecting deficiencies in the level of mRNA in screening for desired transgenic plants, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detecting any number of allelic variants, orthologs or paralog of the gene, and site-directed mutagenesis in eukaryotic cells. The DNA sequences are also useful for recombinant expression of the encoded polypeptides and as immunogens for preparing and screening antibodies. A transgenic plant comprising an expression cassette including a cell cycle regulatory gene is useful for assaying enzyme agonists and antagonists, and as immunogens or antigens to obtain antibodies. The antibodies are useful in assaying expression levels of cell cycle regulatory proteins, for identifying and isolating nucleic acids from expression libraries, for identifying homologues of polypeptides from other species, and for purification of the proteins.

Sequence 1930 BP; 518 A; 501 C; 545 G; 416 T; 0 U; 0 Other;

Sequence 1980 BP; 518 A; 501 C; 545 G; 416 T; 0 U; 0 Other;

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Query Match      12.0%; Score 197; DB 3; Length 1980;
Best Local Similarity 54.9%; Pred. No. 1.8e-41;
Matches 464; Conservative 0; Mismatches 360; Indels 21; Gaps 3;

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490	ATGGGTGCACAGAAACAAAGACATATTAAGACGAAGATGAATTGCTCATGATATTGAC	549
744	AAGGCTCCCTGTGGAAATCACTGATAAGACACGCGAAGTAGCAGTGAATCGAAGACATCGAC	803
550	AGTGACAGATCGGGGAACCGCTTGCTGCAACAGAAATATGTTAAAGAGCTTTACACCTTT	609
804	AAGTTGGACGTCAAATAGAGCTCGAGTTGGATACATTGAGGACATCTACAGGTTG	863
610	TACAGAGAAAATGAGGCTTAAGTTGTGAAGCCAGATTACATGTCCAGACCAACAGAC	669
864	TACAAGATTGCTCAGACATGACAGACGCCCATG---TGAATTATATAGACACCCCAAGTCGAG	920
670	ATTAATCTAAAGATGAGACGAATCTTGATTGACTGCTGATTCAGGTTCACTACAAGTTT	729
921	ATCAACCCCTAAGATGAGGGGTATCTCGGCTGGTTGGATTAATTGAAGTACACCACAAGTTG	980
730	GAACGTGATGGATGAGACGCTCTTTCTTATATGGTAAACATAATAGATAGATTCTTTGGAAGAAG	789
981	GAGCTGATGCGGAAACTCTCTACTTACCACTATGACCATGATCATCATGATCACTCTCGCTG	1040
790	GAAGTGGTTCCAGGAAGAGCTTACAACCTGGTTGGAGTCACAGCTATGCTGCTCGCTTGT	849
1041	CAACCAGTCTCTGGAAGGGAGCTGCAGCTGGTCGGTGTTCAGCTTATGCTGATCGGCTGC	1100
850	AAATATGAGAGAGTATCTGTTCAGTTGTTGAGGACCTTGTTGTTGATATCTGACCGTGCC	909
1101	AAGTACGAGAGATTGGGCCCCAGAGGTCGAACGATTTCTTATATCAGACAGTGA	1160
910	TACACAAAAGGGCAATTTTAGAATAAGAAAAGTTGATTTCTGACACCGTGCAGTTCAAC	969
1161	TACAGCAGGGAGAGATCCCTTTGATGGAGAAAGGAATCTGTAATAGCTGGAGTGGAAAC	1220
970	ATGTCTGTTCACACACCTTATGTCTTCATGAAGAGGTTTCTGAAAGCTGCAG-----	1021
1221	CTCACTGTCCCTACAGTATACATGTTCTCTTTCGTTTCTGAAGCGGCGAGCCTTGGGC	1280
1022	----ATGCAGATAAACAGCTTGAGCTAGCGTCAATTTTTATGCTGGAGCTCTCGTTGGTA	1077
1281	AACAAAGTTGAGAAAAGAGATGGAGAAATAGTCTTCTTCTTCGCTGAACCTGGCGCTGATG	1340
1078	GAATACCAAAATGCTGAATTTATCGGCCCTTCGATCTGGCTGCTGGCGGTTTATACTGCA	1137
1341	CAGTACGGCTTGGTGACCGGGCTGCCCTTCGCTGCTGCTGCTCGTTGTTGCTACGACGCC	1400
1138	CAGTGTGCTATCAATCGTTGCCAGCACTGGACAAAGGCTGCGAGTCTCATATA-----GC	1191
1401	AGGCTCACTCTCAAGAGGGGTCCCTCTGGAACCGACACCCCTCAAGCACCAACGAGGCTTC	1460

PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 10-JUN-1999; 99US-0138847P.
 PR 14-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139452P.
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 PR 17-JUN-1999; 99US-0139492P.
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 PR 08-JUL-1999; 99US-0142803P.
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 PR 20-JUL-1999; 99US-0144332P.
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 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147192P.
 PR 05-AUG-1999; 99US-0147260P.

PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
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 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
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 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
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 PR 07-OCT-1999; 99US-0158023P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
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 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
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 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
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 PR 25-OCT-1999; 99US-0161406P.
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 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 11.7%; Score 191.8; DB 3; Length 1385;
 Best Local Similarity 55.4%; Pred. No. 3.6e-40;

Matches 436; Conservative 0; Mismatches 342; Indels 9; Gaps 3;

QY 536 TCTGATATTTGACAGTGCAGCTGGGGAACCCCTGCTGCAACAGATATTTAAAG 595
 Db 559 TGATCAGATTTGATGCTGTGGATGTAAACATGAATGAATGCTGCTGTGGAATACCTAGAG 618
 QY 596 AGCTTTTACACCTTTTACAGAGAAATGAGGCTTAAGGTTGTAAAGGCCAGATTACATGT 635
 Db 619 ACATCTTCAAGTTTATAG--GACTGTGGAAGGAAGGAGGATTAAGACTATATAG 675
 QY 656 CAGCCCAACAGACATAAATCAAGATGAGAGCAATTTCTGATGACTGGCTGATTGAGG 715
 Db 676 GATCAACACTGAGATAAAGAGAGATGAGATCAATTTCTGATAGATTGGCTTGTAGATG 735
 QY 716 TTCACTACAAGTTTGAACCTGATGAGTGAACGCTCTTTCTTATGGTAAACATAATAGATA 775
 Db 736 TTCACAGGAAGTTTGAAGTTGATGCCAGAGAGCTATATCTTAACCATTAACCTCGTTGATC 795
 QY 776 GATCTTGGNAAGGAGTGTTCACAGGAAGCTACAACTGCTGGAGTCAACGTA 835
 Db 796 GGTTCCTATCTTTGACATGGTTTCATAGAGAGAGCTTCAGCTGTGTGGACTAGTGCTA 855
 QY 836 TGCTGCTCGTTGTAATATGAGGAGGTATCTTTCCAGTTTGTGAGGACCTTGTGCTGA 895
 Db 856 TGCTTATAGTTTCAAGTATGAGGAGATTGGGCTCTGAGGTTAATGATTTCGTCGTA 915
 QY 896 TATCTGACCGTGCCTACACAAAGGCGCAATTTTGAAGATGCAAAAGTTGATTCTGAACA 955
 Db 916 TTTCCGACAAATGCTTATACAGAAACAGGTTTTCGCTATGAGAGAAATCGATCTAGGAC 975
 QY 956 CGTGCAGTTCAACATGTCTGTTCCAAACCTTATGTCTTCATGAAGAGGTTTCTGAAAG 1015
 Db 976 AAGTGAATGGTACATCACTGTGTCCAACTCTTATGTCTTCCGCGATACCTTAAAG 1035
 QY 1016 CTCAGATGCA--GATAAACAGCTTGAGCTAGCTGCTATTTTCATGCTGAGCTCGCT 1072
 Db 1036 CTCGGTTCCATGATGCTGAGATGAGAAATTTGGTCTTACTTGGCTGAGCTGGAC 1095
 QY 1073 TGCTAGATACCAAAATGCTGAAT---ATCGGCTTCGATCTGGCTGCTGCTCGGTTT 1129
 Db 1096 TTATGAGTATCTATAGTTGTCTTAAACCGTCCATCGATGCTGCTGCTCATCGGTTT 1155
 QY 1130 ATACTGCAGATGCTATCAATCGTTGGCCAGCACTGGCAAAAGTCTGCGAGTCTCAT 1189
 Db 1156 ATGCTGGCTGAGTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1215
 QY 1190 GCAGATACATAGCGACCACTGCTGAGTGTGAGAGATGATGATGATTTTCCACAGA 1249
 Db 1216 CTGGCTACTCGGAAGATGAGATTATGAGAGATGCGGAAATGCTGATGAAGTTAAGGACT 1275
 QY 1250 AGCTGGAACCAAGTCACTGCGGTGACAGAGAGATGAGTACCTACAGTTCGGTT 1309
 Db 1276 CGGCTTACAGAGATGAGCTAATAGAGTGTTCAGAGAAATACCTCTCTCAGAAACGCTG 1335
 QY 1310 CGGTGGC 1316
 Db 1336 AAGTTGC 1342

RESULT 10

AAC77911

ID AAC77911 standard; cDNA; 1553 BP.

XX

AC AAC77911;

XX

08-FEB-2001 (first entry)

XX

Human cancer associated gene sequence SEQ ID NO:305.

XX

Human; cancer associated gene; cancer antigen; detection: cancer;
 diagnosis: cytotoxic; proliferative; vulnary; immunomodulatory;
 antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;

KW

dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
 vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 immune disorder; haematopoietic cell disorder; autoimmune disorder;
 allergic reaction; graft versus host disease; organ rejection;
 haemostatic; thrombolytic; cardiovascular disorder; infection;
 neurological disease; drug screening; ss.
 Homo sapiens.
 WO200055350-A1.
 21-SEP-2000.
 08-MAR-2000; 2000WO-US005882.
 12-MAR-1999; 99US-0124270P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Ruben SM;
 WPI; 2000-587533/55.
 P-PSDB; AAB43702.
 Novel isolated nucleic acids comprising sequences encoding peptides
 useful for treating or diagnosing e.g. cancer.

Claim 1; Page 863-864; 2352pp; English.

AAC77607 to AAC78448 encode the human cancer associated proteins given in
 AAB43398 to AAB44239. The proteins can have activities based on the
 tissues and cells the genes are expressed in. Example of activities
 include: cytotoxic; proliferative; vulnary; immunomodulatory;
 antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
 dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 nootropic; vasotropic; antipsoriatic and antiangiogenic. The
 polynucleotides and polypeptides can be used for preventing, treating or
 ameliorating medical conditions and diagnosing pathological conditions.
 Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 the present invention may be used to treat immune disorders by activating
 or inhibiting the proliferation, differentiation or mobilisation of
 immune cells, to treat disorders of haematopoietic cells, autoimmune
 disorders, allergic reactions, graft versus host disease and organ
 rejection, modulate haemostatic or thrombolytic activity, modulate
 inflammation, cancers, cardiovascular disorders, neurological disease and
 bacterial or viral infections. The peptides, nucleotides, antibodies,
 agonists and antagonists may be also used in drug screens. AAC78449 to
 AAC78457 and AAB44240 represent sequences used in the exemplification of
 the present invention

Sequence 1553 BP; 451 A; 351 C; 346 G; 403 T; 0 U; 2 Other;

Query Match 9.9%; Score 161.4; DB 3; Length 1553;
 Best Local Similarity 55.7%; Pred. No. 4.4e-32;
 Matches 328; Conservative 1; Mismatches 257; Indels 3; Gaps 1;

QY 536 TCATGATATTGACAGTGCAGACTCGGGAAACCGCTTGTGCAACAGATATGTTAAAG 595

Db 514 TCAGAGCATTGTAACGAGATTGGGAGAACCTCAGCTCTGCACTGACTACGTTAAGG 573

QY 596 AGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTTAAGCCAGATTACATGT 655

Db 574 ATATCTATCAGTATCTCAGGAGCTGGAGGTTTTCAGTCTCATAACCCACATTTCTTAG 633

QY 656 CCAGCCCAACAGACATAAATCAAGATGAGAGCAATTCATGATGCTGCTGATTGAGG 715

Db 634 ATGG--AAGAGATATAAATGAGCATGCTGCTGCACTCTAGTGGATTGGCTGCTAAG 690

QY 716 TTCCTACAAGTTTGAAGTATGATGATGAGAGCTCTTTCTTATGTTAAACATATAGATA 775

Db 691 TCATCTCAGTTTARGCTTCTGAGAGAGACTCTGTACATGTCGCTTGGCATTTATGATC 750

Qy 776 GATTCTTGGAAAGAAAGTGGTTCCAGGAGAAAGCTAACTGGTTGGAGTCACAGCTA 835
 Db 751 GATTCTTACAGGTTTCCAGGAGTGGTTCCAGGAGAAAGCTTCAATTAGTTGGGATTACTGCTC 810
 Qy 836 TGCTGCTCGCTTGAATATATGAGAGAGTATCTGTTCCAGTGTGTTGAGGACCTTGTGCTGA 895
 Db 811 TGCTCTTGGCTTCAAGTATGAGAGAGTATCTGTTCCAGTGTGTTGAGGACCTTGTGCTGA 870
 Qy 896 TATCTGACCGTGCCTACACAAAGGGCAATTTTGAATATGAAAGTTGATTTCTGAACA 955
 Db 871 TCACAGACAATGCTTATACCAAGTTTCCCAATCCGAGAAATGGAACACTCTAATTTTGAAG 930
 Qy 956 CGCTGCAAGTTCAACATGCTGTGTTCCCAACACCTTATGCTTTCATGAAGAGGTTTCTGAAG 1015
 Db 931 AATTGAATTTGAGTTGGTTCGACCTTCCCACTACACTTCTTAAGCGAGCATCAAG 990
 Qy 1016 CTGCAGATGACAGTAAACAGCTTGAAGTGTGCTGATTTTTCATGCTGGAGCTCTGCTGG 1075
 Db 991 CCGGGAGGTTGATGTTGAACAGACACACTTTAGCCAAAGTATTTGATGGAGCTGACTCTCA 1050
 Qy 1076 TAGAATACCAATGCTGAATTTATCGGCTTTCGCAATCTGGCTGCTGCTGC 1124
 Db 1051 TCGACTATGATGATGTCATTAATCACTCTTCTTAAGTAGGAGCAGCTGC 1099

RESULT 11
 AAH14263
 ID AAH14263 standard; cDNA; 1507 BP.

AC AAH14263;

XX 26-JUN-2001 (first entry)

DT Human cDNA sequence SEQ ID NO:11579.

DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EPI074617-A2.

XX .07-FEB-2001.

XX 28-JUN-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-

XX length cDNAs defined in the specification, and for the detection and/or

XX diagnosis of the abnormality of the proteins encoded by the full-length

XX cDNAs.

XX Claim 8; SEQ ID NO 11579; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-

XX length cDNAs defined in the specification. Where a primer set comprises:

XX (a) an oligo-dr primer and an oligonucleotide complementary to the

XX complementary strand of a polynucleotide which comprises one of the 5602

XX nucleotide sequences defined in the specification, where the

CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH24446 to AAH58893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention

XX Sequence 1507 BP; 427 A; 346 C; 337 G; 397 T; 0 U; 0 Other;

XX Query Match 9.8%; Score 160.2; DB 4; Length 1507;

XX Best Local Similarity 55.7%; Pred. No. 9e-32;

XX Matches 328; Conservative 0; Mismatches 258; Indels 3; Gaps 1;

Qy 536 TCATGATATTGACAGTGCAGACTCGGGAAACCCGCTTGTGCAACAGAAATGTAAAG 595

Db 498 TCGAGACATTTGATTAACGAAGATTGGGAGAACCTCAGCTCTGCAGTACGTTAAG 557

Qy 596 AGCTTTACACCTTTTACAGAGAAATAGGCTTAAGAGTTGTGTAGGCGCAGTACATGT 555

Db 558 ATATCTATCAGTATCTCAGGAGCTGGAGTTTTCAGTCCATTAACCCACATTTCTTAG 617

Qy 656 CCAGCCACACAGACATAAATCAAGATGAGAGCAATTCGATTGACTGGCTGATGAGG 715

Db 618 ATGG--AAAGATATTAATGAGCCATGCGTCCATCCTAGTGGTGGTGTACAG 674

Qy 716 TTCCTACAGTTTGAAGTGTGATGAGAGCGCTCTTTCTTATGTTAAACATAATAGATA 775

Db 675 TCCACTCCAAAGTTTAGGCTTCTGCAGGAGACTCTGTACATGTGCTTGGCATTATGATC 734

Qy 776 GATTCTTGGAAAAGAGTGGTTCCAGGAGAGCTCAACTGTTGAGTGCAGCTACAGCTA 835

Db 735 GATTCTTACAGTTTCAAGTGGTTCAGGAGAGCTTCCCGAAGAGCTCAATTAGTTGGGATTCTGCTC 794

Qy 836 TGCTGCTGCTTGTAAATATGAGGAGGTATCTGTTCCAGTGTGTTGAGACCTTGTGCTGA 895

Db 795 TGCTCTTGGCTTCCAGTATGAGGAGATGTTTCTCCAAATATTGAAGACTTTGTTTACA 854

Qy 896 TATCTGACCGTGCCTTACACAAAGGGCAATTTAGAAATGAAAGTTGATTCTGAACA 955

Db 855 TCACAGACAATGCTTATACCAAGTTCCCAAAATCCGAGAAATGGAAGTTCTAATTTTGAAG 914

Qy 956 CGCTGCAAGTTCAACATGCTGTGTTCCACACACCTTATGCTTTCATGAAGAGGTTTCTGAAG 1015

Db 915 AATTGAATTTGAGTTGGTTCGACCTTGCACACTACACTTCTTAAGGCGGAGCATCAAG 974

Qy 1016 CTGCAGATGACAGTAAACAGCTTGAAGTGTGATGCTATTTTTCATGCTGGAGCTCTGCTGG 1075

Db 975 CCGGGGAGGTTGATGTTGAACAGCACACTTAGCCAAAGTATTTGATGAGGCTGACTCTCA 1034

Qy 1076 TAGAATACCAATGCTGAATTTATCGGCTTTCGCACTCTGCTGCTGCTGC 1124

Db 1035 TCGACTATGATGCTGCTGATTTATCATCTTCTTAAGTAGGAGCAGCAGCTGC 1083

RESULT 12

ACH03960

ID ACH03960 standard; cDNA; 1532 BP.

XX ACH03960;

XX 26-SEP-2003 (first entry)

XX Human cDNA differentially expressed in lung cancer #165.

XX Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;

KW

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX Mus musculus.
XX WO200189188-A2.
XX PD 22-NOV-2001.
XX PF 18-MAY-2001; 2001WO-JP004192.
XX PR 18-MAY-2000; 2000JP-00145977.
XX PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX WPI; 2002-034733/04.
XX DR P-PSDE; ABB57124.
XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX expression levels of particular genes defined in the specification or by
XX determining the expression profile of a gene group comprising these
XX genes.
XX Claim 2; Page 783-786; 2690pp; English.
XX . The present invention describes a method for examining ischaemic
XX conditions, comprising measuring the expression levels of particular
XX genes (I) in a test sample or determining the expression profile of a
XX gene group in the sample comprising genes selected from (I). The method
XX is useful for examining the ischaemic condition (e.g. compressive
XX ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX expression levels of particular genes (ABI99202 to ABI99912, encoding the
XX protein sequences in ABB57020 to ABB57374) or by determining the
XX expression profile of a gene group comprising these genes. The expression
XX levels or expression profiles produced by these genes are used as an
XX indicator when screening for ischaemic condition-improving drugs or
XX therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
XX primers for a mouse ischaemic condition related sequence, which are used
XX in the exemplification of the present invention
SQ Sequence 2308 BP; 631 A; 499 C; 517 G; 661 T; 0 U; 0 Other;

Query Match 9.5%; Score 155.6; DB 6; Length 2308;
Best Local Similarity 55.1%; Pred. No. 1.9e-30;
Matches 327; Conservative 0; Mismatches 284; Indels 3; Gaps 1;

QY 536 TCATGGATATTGACAGTCGAGACTCGGGGAACCCGGTTGCTGCAACAGAGATATGTTAAAG 595
DB 524 TGAGTGACGTAGACGCGAGATGATGGGGCTGACCCAAACCTCTGTAGTGAATATGTGAAG 583
QY 596 AGCTTTACACCTTTTACAGAGAAATGAGCTAAGAGTTGTGTAAGCCAGATTACATGT 655
DB 584 ATATCTATGCTTATCTCCGCAACTGGAGGAGAGAGCTAGTTAGACCAAAATACCTAC 643
QY 656 CCAGCCAAACAGACATAACTCAAAGATGAGAGCAATTCGATTGACTGGCTGATTGAGG 715
DB 644 AGGGTCGTGAAG---TGACTGGAACATGAGAGCTATCCTCATTTGACTGGCTAATACAGG 700
QY 716 TTCACTCAAGTTTGAAGTATGATGAGAGCGCTCTTCTTATGTTGTAACATATAGATA 775
DB 701 TTCAGATGAATTTAGGCTGCTTCAGGAGACCATGTATACATGACTGTGTCTCATTATTGATC 760
QY 776 GATTCTTGGAAAAGGAGTGTTCACAGGAAGAGCTACAACTGGTTGGAGTCACAGCTA 835
DB 761 GGTTCATCCAGACAGATTGTGTGCCCCAAGAGATGCTACAGCTGTGGTGAACGCCCA 820
QY 836 TGCTCTCGCTTGAATATGAGAGAGGTATCTGTTCAGTTGTTGAGGACCTTGCTGA 895
DB 821 TGTTTATTGCAAGCAAAATATGAGGAGATGTACCCCTCCAGAAATAGGTGACTTCGCTTTG 880
QY 896 TATCTGACCGTCTTACACAAAAGGGCAAAATTTAGAAATGGAAGTTGATTCTGAACA 955

DB 881 TGACTTAACACACGTACACTAAGCACACAGATGAGATGAGATGAAGATTCTCAGAG 940
QY 956 CGGTGAGTTCAACATGTCTGTTCCAAACACCTTATGCTTTCATGAAGAGTTTCTGAAAG 1015
DB 941 TTTGAACTTCAGCCTGGGTCGCCCTCTGCTCTGCACTTCTCCGTAGAGCATCTAAG 1000
QY 1016 CTGCAGATGCAGATAAAACAGCTTTGAGCTAGCGTCAATTTTCAATGCTGGAGCTCTGCTGG 1075
DB 1001 TCGGAGAGGTTGACGTCGAGCAGCACACTTTGGCCAAATACCTCATGAGGCTCTCCATGC 1060
QY 1076 TAGAATACCAATGCTGAATTATCGGCCCTTGGCATCTGCTGCTGCTGCGGTTT 1129
DB 1061 TGGACTCGGACATGGTGCAATTTTGTCTCTCTCAAAATTGCAAGCTGGGGCTTTCT 1114

Search completed: March 20, 2004, 20:02:04
Job time : 679 secs

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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 19:36:30 ; Search time 131 Seconds
(without alignments)
6930.532 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1536
Sequence: 1 tcacggggtcttcctcgccg.....aaaaaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY_NUC
Gapex 10.0 , Gapex 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	223.4	13.7	274	4	US-09-313-294A-263
2	160.2	9.8	1375	4	US-10-083-889-21
3	160.2	9.8	1530	4	US-10-083-889-1
4	155.4	9.5	1452	1	US-08-187-785-2
5	155.4	9.5	1452	4	US-09-023-655-1048
6	153.8	9.4	1302	1	US-08-425-299A-1
7	141.6	8.7	1336	4	US-10-083-889-25
8	125.6	7.7	1634	2	US-08-460-895-1
9	125.6	7.7	1634	2	US-09-210-889-1
10	125.6	7.7	1649	2	US-08-692-787-8
11	125.6	7.7	1649	3	US-09-097-199-8
12	125.6	7.7	1649	4	US-09-023-655-1268
13	119.6	7.3	1752	1	US-08-463-090B-4
14	111.6	6.8	826	3	US-09-337-171-12
15	111.6	6.8	826	3	US-09-773-459-12
16	97	5.9	333	4	US-09-023-655-64
17	86.6	5.4	638	3	US-09-328-111-186
18	86.8	5.3	1212	2	US-09-092-770-18
19	86.8	5.3	1212	3	US-09-222-851-18
20	85.6	5.2	1215	3	US-09-092-770-8
21	85.6	5.2	1215	3	US-09-222-851-8
22	72	4.4	1215	2	US-09-092-770-1
23	72	4.4	1215	3	US-09-222-851-1
24	71.4	4.4	1212	2	US-09-092-770-17
25	71.4	4.4	1212	3	US-09-222-851-17
26	69.8	4.3	1212	2	US-09-092-770-2
27	69.8	4.3	1212	3	US-09-222-851-2

28	64	3.9	1214	2	US-09-092-770-7	Sequence 7, Appli
29	64	3.9	1214	3	US-09-222-851-7	Sequence 7, Appli
30	59.8	3.7	273	4	US-09-313-294A-1848	Sequence 1848, Ap
C 31	58.4	3.6	532	4	US-09-389-681-432	Sequence 432, App
C 32	58.4	3.6	532	4	US-09-620-405B-432	Sequence 432, App
C 33	58.4	3.6	532	4	US-09-433-826B-432	Sequence 432, App
C 34	58.4	3.6	532	4	US-09-604-287A-432	Sequence 432, App
C 35	58.4	3.6	532	4	US-09-834-759-432	Sequence 432, App
36	58.2	3.6	1101	3	US-08-895-707-5	Sequence 5, Appli
37	58.2	3.6	1158	3	US-08-895-707-8	Sequence 8, Appli
38	58.2	3.6	1179	1	US-08-706-539-3	Sequence 3, Appli
39	58.2	3.6	1179	3	US-09-027-007-3	Sequence 3, Appli
40	58.2	3.6	1188	1	US-08-706-539-2	Sequence 2, Appli
41	58.2	3.6	1188	3	US-09-027-007-2	Sequence 2, Appli
42	58.2	3.6	1311	1	US-08-706-539-4	Sequence 4, Appli
43	58.2	3.6	1311	3	US-09-027-007-4	Sequence 4, Appli
44	58.2	3.6	1680	1	US-08-706-539-1	Sequence 1, Appli
45	58.2	3.6	1680	1	US-08-522-166-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-313-294A-263
; Sequence 263, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 263
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700548873H1
US-09-313-294A-263

Query Match	13.7%	Score	223.4	DB	4	Length	274
Best Local Similarity	93.5%	Pred. No.	1.6e-52				
Matches	244	Conservative	0	Mismatches	16	Indels	1
						Gaps	1
QY	627	TAAGAGTTCTGTAAGCCAGATTACATGTCACAGCAACAAAGACATAAACTCAAAGATGAG	686				
DB	1	TAAGAGTTCTGTAAGCCAGATTACATGTCACAGCAACAAAGACATAAACTCAAAGATGAG	60				
QY	687	AGCAATTCCTGATGAGTGGCTGATTCAGTTGAGTTCACTACAGTTTGAATGATGATGAGAC	746				
DB	61	AGCAATTCCTGATGAGTGGCTGATTCAGTTGAGTTCACTACAGTTTGAATGATGATGAGAC	120				
QY	747	GCTCTTCTTATGGTAACATATAGATGATCTTGGAAAGGAAGTGGTTCCAAAGAA	806				
DB	121	GCTATTTCTTACGTAACATGATGATCTTGGAAAGGAAGTGGTTCCAAAGAA	180				
QY	807	GAAGCTACAACTGGTTGGAGTCAACAGCTATGCTGCTTAAATATGAGGAGTATC	866				
DB	181	GAAGCTACAACTGGTTGGAGTCAACAGCTATGCTGCTTAAATATGAGGAGTATC	239				
QY	867	TGTTCCAGTTGTTGAGGACCT	887				
DB	240	AGTTCCAGTTGTTGAGGACCT	260				

RESULT 2
US-10-083-889-21

; Sequence 21, Application US/10083889
; Patent No. 6573894
; GENERAL INFORMATION:
; APPLICANT: Zahner, Joseph E.
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
; FILE REFERENCE: 16850-7331
; CURRENT APPLICATION NUMBER: US/10/083,889
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/271,798
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 21
; LENGTH: 1375
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-083-889-21

Query Match 9.8%; Score 160.2; DB 4; Length 1375;
Best Local Similarity 55.7%; Pred. No. 1.6e-34;
Matches 328; Conservative 0; Mismatches 258; Indels 3; Gaps 1;

QY 536 TCATGGATATTCAGATGCGAGCTCGGGGAACCGCTTCTGCTCAACAGATATGTTAAAG 595
DB 528 TCGAGGACATTTGATAACCAAGATTGGGAGAACCCCTCAGCTCTGCAGTGACTACGTTAAAG 587
QY 596 AGCTTTACACCTTTTACAGAGAAAATGAGGCTAAGAGTTGTGTAAAGCCAGATTACATGT 655
DB 588 ATATCTATCATGTAATCTCAGGCGAGCTGGAGGTTTTCAGTCCATTAACCCACATTTCTTAG 647
QY 656 CCAGCCACAGACATTAAGTCAAGATGAGAGCAATCTGATGAGTCTGCTGAGTGAAG 715
DB 648 ATGG---AAGAGATATAAATGAGCGCATGCGTGCATCCCTAGTGGATTGGCTGGTACAAG 704
QY 716 TTCCTACCAAGTTTGAATGATGATGAGAGCTCTTCTTATGTTAAACATAATAGATA 775
DB 705 TCCACTCCAAGTTTAGGCTTCTGAGGAGACTCTGTACATGTGCGTTGGCATTTATGATC 764
QY 776 GATCTTGGAAAAGAGTGTTCAGAGGAAGAGCTACAACTGTTGAGTGCAGCTA 835
DB 765 GATTTTACAGGTTTACAGCCAGTTTCCCGAAGAGAGCTTCAATAGTTGGGATTTACTGCTC 824
QY 836 TGCTCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGCTGTA 895
DB 825 TGCTCTCGCTTCCAGATGATGAGGAGATGTTTCTCCAAATATTGAGACTTTGTTTACA 884
QY 896 TATCTGACCGTGCCTACACAAAGGGCAATTTTAGAAATGGAAGTTGATTTCTGAACA 955
DB 885 TCACAGACAATGCTTATACCAAGTTCCTCAATTCGAGAAATGGAAACTCTTAATTTTGAAG 944
QY 956 CGCTGCAATTCATGCTGCTTCCAAACACCTTATGTTCTCATGAAGAGGTTTCTGAAAG 1015
DB 945 AATTGAAATTTGAGTTGGTTCGACCTTGGCCACTACACTTCTTAAGCGAGCATCAAAAG 1004
QY 1016 CTGAGATGAGATAAAGAGCTTGGCTGAGCTAGGCTATTTTCATGCTGGAGCTGCTGG 1075
DB 1005 CCGGGAGGTTGATTTGACACAGCACTTTAGCCAAAGTATTGATGGAGCTGACTCTCA 1064
QY 1076 TAGAATACCAATGCTGAATTCGGCTTCGCACTTGGCTGCTGCTGC 1124
DB 1065 TCGACTATGATATGTTGCTGATTTATCATCTTCTTAAGGTAGCAGAGCTGC 1113

RESULT 3
US-10-083-889-1
; Sequence 1, Application US/10083889
; Patent No. 6673894
; GENERAL INFORMATION:
; APPLICANT: Zahner, Joseph E.
; TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
; FILE REFERENCE: 16850-7331
; CURRENT APPLICATION NUMBER: US/10/083,889
; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: US 60/271,798
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Liu, J.H.
; AUTHORS: Wei, S.
; AUTHORS: Burnette, P.K.
; AUTHORS: Camero, A.M.
; AUTHORS: Hutton, M.
; AUTHORS: Djou, J.Y.
; TITLE: Functional association of TGF-beta receptor II with cyclin B
; JOURNAL: Oncogene
; VOLUME: 18
; ISSUE: 1
; PAGES: 269-275
; DATE: 1999-01-07
; DATABASE ACCESSION NUMBER: Genbank Accession No. 6673894 NM_004701
; DATABASE ENTRY DATE: 2000-11-01
; US-10-083-889-1

Query Match 9.8%; Score 160.2; DB 4; Length 1530;
Best Local Similarity 55.7%; Pred. No. 1.7e-34;
Matches 328; Conservative 0; Mismatches 258; Indels 3; Gaps 1;

QY 536 TCATGGATATTCAGATGCGAGCTCGGGGAACCGCTTCTGCTCAACAGATATGTTAAAG 595
DB 498 TCGAGGACATTTGATAACCAAGATTGGGAGAACCCCTCAGCTCTGCAGTGACTACGTTAAAG 557
QY 596 AGCTTTACACCTTTTACAGAGAAAATGAGGCTAAGAGTTGTGTAAAGCCAGATTACATGT 655
DB 558 ATATCTATCATGTAATCTCAGGCGAGCTGGAGGTTTTCAGTCCATTAACCCACATTTCTTAG 617
QY 656 CCAGCCACAGACATTAAGTCAAGATGAGAGCAATCTGATGAGTCTGCTGAGTGAAG 715
DB 618 ATGG---AAGAGATATAAATGAGGAGCTGCGTGCATCCCTAGTGGTGGTACAAG 674
QY 716 TTCCTACCAAGTTTGAATGATGATGAGAGCTCTTCTTATGTTAAACATAATAGATA 775
DB 675 TCCACTCCAAGTTTAGGCTTCTGAGGAGACTCTGTACATGTGCGTTGGCATTTATGATC 734
QY 776 GATCTTGGAAAAGAGTGTTCAGAGGAAGAGCTACAACTGTTGAGTGCAGCTA 835
DB 735 GATTTTACAGGTTTACAGCCAGTTTCCCGAAGAGAGCTTCAATAGTTGGGATTTACTGCTC 794
QY 836 TGCTCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGCTGTA 895
DB 795 TGCTCTCGCTTCCAAAGTATGAGGAGATGTTTCTCCAAATATTGAAGACTTTGTTTACA 854
QY 896 TATCTGACCGTGCCTACACAAAGGGCAATTTTAGAAATGGAAGTTGATTTCTGAACA 955
DB 855 TCACAGACAATGCTTATACCAAGTTCCTCAATTCGAGAAATGGAAGTCTTAATTTTGAAG 914
QY 956 CGCTGCAATTCATGCTGCTTCCAAACACCTTATGTTCTCATGAAGAGGTTTCTGAAAG 1015
DB 915 AATTGAAATTTGAGTTGGTTCGACCTTCCCACTACACTCTTCTTAAGGCGAGCATCAAAAG 974
QY 1016 CTGAGATGAGATAAAGAGCTTGGCTGAGCTATTTTTCATGCTGGAGCTGCTGCTGG 1075
DB 975 CCGGGAGGTTGATTTGACACAGCACTTTAGCCAAAGTATTGATGAGGCTGACTCTCA 1034
QY 1076 TAGAATACCAATGCTGAATTTATGCGCTTCGCACTCTGCTGCTGCTGC 1124
DB 1035 TCGACTATGATATGTTGCTGATTTATCATCTTCTTAAGGTAGCAGAGCTGC 1083

RESULT 4
US-08-187-785-2
; Sequence 2, Application US/08187785

Patent No. 5756476
GENERAL INFORMATION:
APPLICANT: Epstein, Stephen
APPLICANT: Unger, Ellis
APPLICANT: Speir, Edith
TITLE OF INVENTION: Inhibition of No. 5756476-Transformed Cell Proliferation Using Anti-Sense Oligonucleotides
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,785
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,415
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH001.001A
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human
IMMEDIATE SOURCE:
CLONE: Cyclin B1 cDNA clone
US-08-187-785-2

Query Match 9.5%; Score 155.4; DB 1; Length 1452;
Best Local Similarity 54.7%; Pred. No. 3.6e-33;
Matches 331; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

QY 536 TCATGGATATGACAGTCGAGCTCGGGGAACCGCTTGTGCAACAGAAATATGTTAAAG 595
DB 547 TAAATGATGTCGATGAGAGATGGAGCTGATCAAAACCTTTGTAGTGAATATGTAAG 606
QY 596 AGCTTACACTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAGCCAGATTACATGT 655
DB 607 ATATTATGCTTATCTGAGCACTTGGAGAGGCAAGCAGTCACCAACCAATACCTAC 666
QY 656 CCAGCCCAACAGACATAAACTCAAGATGAGCAAAATCTGTATGATGCTGCTGATTGAGG 715
DB 667 TGGTGGGGAAG--TCACTGGAACATGAGAGCCATCTTAATGATGCTGCTGATTACAGG 723
QY 716 TTCACTACAGTTGAAGTATGATGATGAGCGCTTTCTTATGTTGAACATATAGATA 775
DB 724 TTCAATGAATTCAGGTGTTGGAGGACCATGTACATGCTGCTCAATATTATTAATC 783
QY 776 GATTCTTTGGAAGGAAGTGGTTCCAGGGAAGAGCTACAACTGGTGGAGTCACAGCTA 835
DB 784 GGTTCATCGAATAATTTGTGTGCCCAAGAGATGCTGCAGCTGGTGTGTCCTGCCA 843

QY 836 TGCTGCTGCTTGTAAATATGAGGAGTATCTGTTCCAGTTGTTGAGGACCTTGCTGCTGA 895
DB 844 TGTTTATTCGAAGCAATATGAAGAAATGTACCTCCAGAAATGGTGACTTGTCTTTG 903
QY 896 TATCTGACCGTGCCTACACAAAAGGCAATTTTAGAAATGGAAGTTGATTTCTGAACA 955
DB 904 TGACTGACAACTTATATCTAAGCAACCAATCAGACAGATGGAATGAAGATTTCTAAGAG 963
QY 956 CGCTGCAGTTCAACATGCTGTTTCCAAACACCTTATCTCTTCAATGAAGAGTTTCTGAAAG 1015
DB 964 CTTTAAACTTTGGTCTGGGTGCGGCTCTACCTTTCACITTCCTTGGAGAGCATCTTAAGA 1023
QY 1016 CTGCAGATGAGATAAAGAGCTTGACCTAGCTGCTATTTTCATGCTGGAGCTCTGCTTGG 1075
DB 1024 TTGGAGAGTTGATGTCGAGCAACATCTTTGGCCAAATACCTGTATGGAACCTAATATGT 1083
QY 1076 TAGAATACCAAAATGCTGAATATTCGGCTTTCGATCTGGCTGCTGCTGGGTTTATFAC 1135
DB 1084 TGGACTATGACATGGTGCACTTTCTCCCTCTCTCAATTCGACAGGAGCTTTTGGCTTAG 1143
QY 1136 CACAG 1140
DB 1144 CACTG 1148

RESULT 5
US-09-023-655-1048
Sequence 1048, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1048:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g181243
US-09-023-655-1048

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Query Match      9.5%; Score 155.4; DB 4; Length 1452;
Best Local Similarity 54.7%; Pred. No. 3.6e-33;
Matches 331; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

QY 536 TCATGGATATTCAGAGTGCAGTTCGGGACCCGCTTGTCTGCAACAGAAATATGTTAAAG 595
Db 547 TAAATGATGTGGATGCAAGATGAGCTGATCCAAACCTTTGTAGTGAATGTTGAAAG 606
QY 596 AGCTTTACACCTTTTACAGAGAAATGAGGCTAGAGTTGTGTAAGGCCAGATTACATGT 555
Db 607 ATATTATGCTTATCTGAGACAACTTGGGAAGAGCAGCTGACCAAAATACCTTAC 666
QY 656 CCAGCCAAACAGACATAAATCTCAAAGATGAGCAATTCGTATGCTGGCTGATGAGG 715
Db 667 TGGGTTCGGGAAG---TCACTGGAACATGAGAGCCATCTTAATTGCTGCTAGTACAGG 723
QY 716 TTCACTCAAGTTTGAACCTGATGATGAGAGCTCTTCTTCTTATGTTAAACATAATAGATA 775
Db 724 TTCAATGAATTCAGGTTGTTGAGGAGACCAATGATGATGCTGCTCATTATGATC 783
QY 776 GATTCCTGGAAAGAAAGTGGTTCCAAAGGAAGCTACAACTGGTTGAGTCAAGCTA 835
Db 784 GGTTTCATGCAAAATTAATTGTGTGCCCAAGAGATGCTGAGCTGGTTGCTGCTCACTGCCA 843
QY 836 TGCTGCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGA 895
Db 844 TGTATTTCGAAGCAATATGAAGAAATGTACCTCCAGAAATTTGGTACTTTGCTTTG 903
QY 896 TATCTGACCGTGCCTACACAAAGGGGCAATTTTGAATGGAAGTGTGTTCTGAACA 955
Db 904 TGACTGCAACACATTAATGCAAGCAACCAATTCAGAGATGGAATGGAAGATTTAAAG 963
QY 956 CGCTGCAAGTTCAACATGCTGTGTTCCAAACCTTATGTTCTATGAAGAGGTTTCTGAAAG 1015
Db 964 CTTTAAACTTTGCTGGTGGGCTCTACTCTTTGCACTTCTCTCGAGAGCATCTAAGA 1023
QY 1016 CTGAGATGAGATTAACACCTTGAAGTACGCTGATGCTGCTGCTGCTGCTGCTGCTG 1075
Db 1024 TTGAGAGGTTGATGTCGAGCAACATATCTTGGCCAAATACCTGATGGAACATAATGT 1083
QY 1076 TAGAATACCAATGCTGAATATTCGGCTTCGCACTGCTGCTGCTGCTGCTGCTGCTG 1135
Db 1084 TGGACTATGACATGGTGCACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1143
QY 1136 CACAG 1140
Db 1144 CACTG 1148

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RESULT 6
US-08-425-299A-1
; Sequence 1, Application US/08425299A
; Patent No. 5726025
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: King, Randall W.
; APPLICANT: Peters, Jean-Michael
; TITLE OF INVENTION: Assay and Reagents for Detecting Inhibitors
; TITLE OF INVENTION: of Ubiquitin-Dependent Degradation of
; TITLE OF INVENTION: Cell Cycle Regulatory Proteins
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,299A
FILING DATE: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1299
US-08-425-299A-1

Query Match      9.4%; Score 153.8; DB 1; Length 1302;
Best Local Similarity 54.5%; Pred. No. 9.5e-33;
Matches 330; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

QY 536 TCATGGATATTCAGAGTGCAGTTCGGGACCCGCTTGTCTGCAACAGAAATATGTTAAAG 595
Db 458 TAAATGATGTGGATGCAAGATGAGCTGATCCAAACCTTTGTAGTGAATGTTGAAAG 517
QY 596 AGCTTTACACCTTTTACAGAGAAATGAGGCTTAAAGTTGTGTAAGGCCAGATTACATGT 655
Db 518 ATATTATGCTTATCTGAGACAACTTGGGAAGAGCAGCTGACGCCAAATACCTTAC 577
QY 656 CCAGCCAAACAGACATAAATCTCAAAGATGAGAGCAATTCGTATGCTGGCTGATGAGG 715
Db 578 TGGGTTCGGGAAG---TCACTGGAACATGAGAGCCATCTTAATTGCTGCTAGTACAGG 634
QY 716 TTCACTCAAGTTTGAACCTGATGAGAGCTCTTCTTCTTATGTTAAACATAATAGATA 775
Db 635 TTCAATGAATTTCAAGTTTGTGAGGAGACCATGATGATGCTCTCCATTATGATC 694
QY 776 GATTCCTGGAAAGGAAGTGGTTCCAAAGGAAGCTACAACTGGTTGGAGTCAAGCTA 835
Db 695 GGTTCATGCAAGAAATATGTTGCCCAAGAGATGCTGAGCTGGTTGGTGTCACTGCCA 754
QY 836 TGCTGCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGA 895
Db 755 TGTATTTCGAAGCAATATGAAGAAATGTACCTCCAGAAATTTGGTGACTTTGCTTTG 814
QY 896 TATCTGACCGTGCCTACACAAAGGGGCAATTTTGAATGGAAGTGTGATTTCTGACA 955
Db 815 TGACTGCAACACATTAATGCTAAGCACCACCAATCAGACAGATGGAATGAAGATTCTTAAG 874
QY 956 CGCTGCAAGTTCAACATGCTGTTCACACACCTTATGCTTCTCATGAAGAGGTTTCTGAAAG 1015
Db 875 CTTTAAACTTTGCTGGGTGGGCTCTTACCTTTGCACTTCTCTCGAGAGCATCTAAGA 934
QY 1016 CTGAGATGCAAGATAAAGCTTGTAGCTAGGCTGCTATTTTTCATGCTGGAGCTTGTCTGG 1075
Db 935 TTGAGAGGTTGATGTCGAGCAACATATCTTTGGCCAAATACCTGATGAACTAATATCT 994
QY 1076 TAGAATACCAATGCTGAATATTCGGCTTTCGCATCTGCTGCTGCTGCTGCTGCTGCTG 1135
Db 995 TGGACTATGACATGGTGCACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1054
QY 1136 CACAG 1140
Db 1055 CACTG 1059

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RESULT 7
US-10-083-889-25
Sequence 25, Application US/10083889
Patent No. 6673894
GENERAL INFORMATION:
APPLICANT: Zahner, Joseph E.
TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
FILE REFERENCE: 16850-7331
CURRENT APPLICATION NUMBER: US/10/083,889
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/271,798
PRIOR FILING DATE: 2001-02-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Word 97
SEQ ID NO 25
LENGTH: 1336
TYPE: DNA
ORGANISM: Mus musculus
US-10-083-889-25

Query Match 8.7%; Score 141.6; DB 4; Length 1336;
Best Local Similarity 55.7%; Pred. No. 2.4e-29;
Matches 292; Conservative 0; Mismatches 229; Indels 3; Gaps 1;
QY 583 GAATATGTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTAAGAGTTGTGAAGG 642
DB 530 GAATATGTTAAAGATATCTATGCTTATCTCCGACAACTGGAGGAGAGCAGTCAGTTAGA 589
QY 643 CCAGATTCATGTCGAGCAACAGACATAAATCTCAAGATGAGCAATCTCATTTGAC 702
DB 590 CCAGAAATACCTACAGGTCGTGAAG---TGACTGGAACATGAGAGTATCTCTCATTTGAC 646
QY 703 TGGCTGATTGAGTTCACTACAAAGTTTGAACATGATGATGAGAGCTCTTTCTTATGGTA 762
DB 647 TGGCTAATACAGTTTCAGATGAATTTAGGCTGCTTCAGGAGACCATGTACATGACTGTG 706
QY 763 AACATAATAGATAGATTTCTGGAAGAGAGAGTGTTCAGAGAGAGAGCTACACTGTT 822
DB 707 TCCATTATATGATCGGTTTCATCAGAACAGTTGTGTGCCAAGAGATGATACAGCTGGTC 766
QY 823 GGAGTCACAGCTATGCTGCTGCTGTTGTAATATGAGGAGGTATCTGTTCCAGTTGTTGAG 882
DB 767 GGTGTAAAGCGCATGTTTATGCAAGCAATATGAGACATGTACCCACAGAAATAGGT 826
QY 883 GACCTTGTGCTGATATCTGACCGTCCCTACACAAAGGGGAAAATTTAGAAATGGAAG 942
DB 827 GACTTCGCTTTGTGACTAAACACACGTCATCACTAAGCACCCAGATCAGACATGGAGATG 886
QY 943 TTGATTTCTGAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
DB 887 AGATTTCTGAGGTTCTGAACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 946
QY 1003 AGTTTCTGAAAGCTGCGAGATGCGATGAGATGAGATGAGATGAGATGAGATGAGATG 1062
DB 947 AGAGCATCTAAAGTCGGAGAGGTTGACGTCAGGAGAGACACTCTGCGCAATACCTCATG 1006
QY 1063 GAGCTCTGCTGTTGATGATACCAATGCTGATTTATCGGCTTC 1106
DB 1007 GAGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050

RESULT 8
US-08-460-895-1
Sequence 1, Application US/08460895
Patent No. 5849508
GENERAL INFORMATION:
APPLICANT: BRECHOT, Christian
APPLICANT: WANG, Jian
APPLICANT: CHENIVESSE, Xavier
APPLICANT: HENGLER, Berthold
APPLICANT: ZINDY, Fr. d. rige
TITLE OF INVENTION: NEW HUMAN CYCLIN A COMPOSITIONS AND A PROCESS FOR THEIR PRODUCTION
NUMBER OF SEQUENCES: 1

Query Match 8.7%; Score 125.6; DB 2; Length 1634;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
QY 529 GAATGCTCATGATGATTTGACAGTGGAGCTCGGGGACCCCTTGTCTGCAACAGATAT 588
DB 571 GACATGCTCAATTTGATTTAGAGATGAAAGCCAGTGTGTTAATGAAGTACCGACTAC 630
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTTAAGAGTTGTGAAGGCCAGAT 648
DB 631 CATGAGATTTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTTAAGTGGT 690
QY 649 TACATGCTCAGCCCAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATGACTGGCTG 708
DB 691 TACATGAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCTCTGAGCTGGTTA 750
QY 709 ATTGAGTTTCACTACAGTTTGAAGTATGAGAGCTCTTCTTATGTTAAACATA 768
DB 751 GTTGAAGTATGAGAGAAATATAAATACAGATGAGAGCTTGTGCTGTGACTAC 810
QY 769 ATAGATAGATTTCTTGAAAGGAGGTTTCCAGGAGAAAGCTACAACTGTTGGAGTC 828
DB 811 ATTGATAGTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 870
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGAGGATCTGTTCCAGTCTTCTGAGGACCTT 888
DB 871 GCTGCTATGCTGTTTGAAGGTTTGAAGAAATATACCCCGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGGCAAAATTTAGAAATGGAAGTTGATT 948
DB 931 GTGTACATTTACAGATCATACCTACACCAAGAAACAAAGTTCTGAGAATGGAGCATCTAG 990
QY 949 CTGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 991 TTGAAAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1050
QY 1006 TTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065

Query Match 7.7%; Score 125.6; DB 2; Length 1634;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
QY 529 GAATGCTCATGATGATTTGACAGTGGAGCTCGGGGACCCCTTGTCTGCAACAGATAT 588
DB 571 GACATGCTCAATTTGATTTAGAGATGAAAGCCAGTGTGTTAATGAAGTACCGACTAC 630
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTTAAGAGTTGTGAAGGCCAGAT 648
DB 631 CATGAGATTTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTTAAGTGGT 690
QY 649 TACATGCTCAGCCCAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATGACTGGCTG 708
DB 691 TACATGAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCTCTGAGCTGGTTA 750
QY 709 ATTGAGTTTCACTACAGTTTGAAGTATGAGAGCTCTTCTTATGTTAAACATA 768
DB 751 GTTGAAGTATGAGAGAAATATAAATACAGATGAGAGCTTGTGCTGTGACTAC 810
QY 769 ATAGATAGATTTCTTGAAAGGAGGTTTCCAGGAGAAAGCTACAACTGTTGGAGTC 828
DB 811 ATTGATAGTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 870
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGAGGATCTGTTCCAGTCTTCTGAGGACCTT 888
DB 871 GCTGCTATGCTGTTTGAAGGTTTGAAGAAATATACCCCGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGGCAAAATTTAGAAATGGAAGTTGATT 948
DB 931 GTGTACATTTACAGATCATACCTACACCAAGAAACAAAGTTCTGAGAATGGAGCATCTAG 990
QY 949 CTGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 991 TTGAAAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1050
QY 1006 TTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065

Query Match 7.7%; Score 125.6; DB 2; Length 1634;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
QY 529 GAATGCTCATGATGATTTGACAGTGGAGCTCGGGGACCCCTTGTCTGCAACAGATAT 588
DB 571 GACATGCTCAATTTGATTTAGAGATGAAAGCCAGTGTGTTAATGAAGTACCGACTAC 630
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTTAAGAGTTGTGAAGGCCAGAT 648
DB 631 CATGAGATTTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTTAAGTGGT 690
QY 649 TACATGCTCAGCCCAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATGACTGGCTG 708
DB 691 TACATGAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCTCTGAGCTGGTTA 750
QY 709 ATTGAGTTTCACTACAGTTTGAAGTATGAGAGCTCTTCTTATGTTAAACATA 768
DB 751 GTTGAAGTATGAGAGAAATATAAATACAGATGAGAGCTTGTGCTGTGACTAC 810
QY 769 ATAGATAGATTTCTTGAAAGGAGGTTTCCAGGAGAAAGCTACAACTGTTGGAGTC 828
DB 811 ATTGATAGTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 870
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGAGGATCTGTTCCAGTCTTCTGAGGACCTT 888
DB 871 GCTGCTATGCTGTTTGAAGGTTTGAAGAAATATACCCCGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGGCAAAATTTAGAAATGGAAGTTGATT 948
DB 931 GTGTACATTTACAGATCATACCTACACCAAGAAACAAAGTTCTGAGAATGGAGCATCTAG 990
QY 949 CTGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 991 TTGAAAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1050
QY 1006 TTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065

Query Match 7.7%; Score 125.6; DB 2; Length 1634;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
QY 529 GAATGCTCATGATGATTTGACAGTGGAGCTCGGGGACCCCTTGTCTGCAACAGATAT 588
DB 571 GACATGCTCAATTTGATTTAGAGATGAAAGCCAGTGTGTTAATGAAGTACCGACTAC 630
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTTAAGAGTTGTGAAGGCCAGAT 648
DB 631 CATGAGATTTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTTAAGTGGT 690
QY 649 TACATGCTCAGCCCAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATGACTGGCTG 708
DB 691 TACATGAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCTCTGAGCTGGTTA 750
QY 709 ATTGAGTTTCACTACAGTTTGAAGTATGAGAGCTCTTCTTATGTTAAACATA 768
DB 751 GTTGAAGTATGAGAGAAATATAAATACAGATGAGAGCTTGTGCTGTGACTAC 810
QY 769 ATAGATAGATTTCTTGAAAGGAGGTTTCCAGGAGAAAGCTACAACTGTTGGAGTC 828
DB 811 ATTGATAGTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 870
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGAGGATCTGTTCCAGTCTTCTGAGGACCTT 888
DB 871 GCTGCTATGCTGTTTGAAGGTTTGAAGAAATATACCCCGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGGCAAAATTTAGAAATGGAAGTTGATT 948
DB 931 GTGTACATTTACAGATCATACCTACACCAAGAAACAAAGTTCTGAGAATGGAGCATCTAG 990
QY 949 CTGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 991 TTGAAAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1050
QY 1006 TTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065

Query Match 7.7%; Score 125.6; DB 2; Length 1634;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
QY 529 GAATGCTCATGATGATTTGACAGTGGAGCTCGGGGACCCCTTGTCTGCAACAGATAT 588
DB 571 GACATGCTCAATTTGATTTAGAGATGAAAGCCAGTGTGTTAATGAAGTACCGACTAC 630
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTTAAGAGTTGTGAAGGCCAGAT 648
DB 631 CATGAGATTTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTTAAGTGGT 690
QY 649 TACATGCTCAGCCCAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATGACTGGCTG 708
DB 691 TACATGAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCTCTGAGCTGGTTA 750
QY 709 ATTGAGTTTCACTACAGTTTGAAGTATGAGAGCTCTTCTTATGTTAAACATA 768
DB 751 GTTGAAGTATGAGAGAAATATAAATACAGATGAGAGCTTGTGCTGTGACTAC 810
QY 769 ATAGATAGATTTCTTGAAAGGAGGTTTCCAGGAGAAAGCTACAACTGTTGGAGTC 828
DB 811 ATTGATAGTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 870
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGAGGATCTGTTCCAGTCTTCTGAGGACCTT 888
DB 871 GCTGCTATGCTGTTTGAAGGTTTGAAGAAATATACCCCGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGGCAAAATTTAGAAATGGAAGTTGATT 948
DB 931 GTGTACATTTACAGATCATACCTACACCAAGAAACAAAGTTCTGAGAATGGAGCATCTAG 990
QY 949 CTGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 991 TTGAAAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1050
QY 1006 TTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065

Query Match 7.7%; Score 125.6; DB 2; Length 1634;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
QY 529 GAATGCTCATGATGATTTGACAGTGGAGCTCGGGGACCCCTTGTCTGCAACAGATAT 588
DB 571 GACATGCTCAATTTGATTTAGAGATGAAAGCCAGTGTGTTAATGAAGTACCGACTAC 630
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTTAAGAGTTGTGAAGGCCAGAT 648
DB 631 CATGAGATTTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTTAAGTGGT 690
QY 649 TACATGCTCAGCCCAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATGACTGGCTG 708
DB 691 TACATGAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCTCTGAGCTGGTTA 750
QY 709 ATTGAGTTTCACTACAGTTTGAAGTATGAGAGCTCTTCTTATGTTAAACATA 768
DB 751 GTTGAAGTATGAGAGAAATATAAATACAGATGAGAGCTTGTGCTGTGACTAC 810
QY 769 ATAGATAGATTTCTTGAAAGGAGGTTTCCAGGAGAAAGCTACAACTGTTGGAGTC 828
DB 811 ATTGATAGTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 870
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGAGGATCTGTTCCAGTCTTCTGAGGACCTT 888
DB 871 GCTGCTATGCTGTTTGAAGGTTTGAAGAAATATACCCCGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGGCAAAATTTAGAAATGGAAGTTGATT 948
DB 931 GTGTACATTTACAGATCATACCTACACCAAGAAACAAAGTTCTGAGAATGGAGCATCTAG 990
QY 949 CTGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 991 TTGAAAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1050
QY 1006 TTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065

Query Match 7.7%; Score 125.6; DB 2; Length 1634;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
QY 529 GAATGCTCATGATGATTTGACAGTGGAGCTCGGGGACCCCTTGTCTGCAACAGATAT 588
DB 571 GACATGCTCAATTTGATTTAGAGATGAAAGCCAGTGTGTTAATGAAGTACCGACTAC 630
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGCTTAAGAGTTGTGAAGGCCAGAT 648
DB 631 CATGAGATTTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTTAAGTGGT 690
QY 649 TACATGCTCAGCCCAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATGACTGGCTG 708
DB 691 TACATGAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCTCTGAGCTGGTTA 750
QY 709 ATTGAGTTTCACTACAGTTTGAAGTATGAGAGCTCTTCTTATGTTAAACATA 768
DB 751 GTTGAAGTATGAGAGAAATATAAATACAGATGAGAGCTTGTGCTGTGACTAC 810
QY 769 ATAGATAGATTTCTTGAAAGGAGGTTTCCAGGAGAAAGCTACAACTGTTGGAGTC 828
DB 811 ATTGATAGTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 870
QY 829 ACAGCTATGCTGCTGCTTGTAAATATGAGAGGATCTGTTCCAGTCTTCTGAGGACCTT 888
DB 871 GCTGCTATGCTGTTTGAAGGTTTGAAGAAATATACCCCGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGGCAAAATTTAGAAATGGAAGTTGATT 948
DB 931 GTGTACATTTACAGATCATACCTACACCAAGAAACAAAGTTCTGAGAATGGAGCATCTAG 990
QY 949 CTGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
DB 991 TTGAAAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1050
QY 1006 TTCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065

Db 1051 TTCTGATCAGCAGCCTGCAAACTGCAAGTTGAAAGTTAGCAATGTTTTGGGAGAA 1110
QY 1066 CTCCTCTGGTAGAAT---ACCAATGCTGAATTATGCGCTTCGCATCTGGCTGCTGCT 1122
Db 1111 TTAAGTTTGAATAGTGTGACCATACCTCAAGTATTTGCCATCAGTTATGCTGGAGCT 1170
QY 1123 GCGGTTTATCTGACAGTGTGCTATCA 1150
Db 1171 GCCTTTTATCTGACACTCTACACAGTCA 1198

RESULT 9

US-09-210-889-1
; Sequence 1, Application US/09210889
; Patent No. 6103887
; GENERAL INFORMATION:
; APPLICANT: BRECHOT, Christian
; APPLICANT: WANG, Jian
; APPLICANT: CHENIVESSE, Xavier
; APPLICANT: HENGLEIN, Berthold
; APPLICANT: ZINDY, Fr d rique
; TITLE OF INVENTION: NEW HUMAN CYCLIN A COMPOSITIONS AND A
; TITLE OF INVENTION: PROCESS FOR THEIR PRODUCTION, THE CORRESPONDING NUCLEOTIDE SEQ
; TITLE OF INVENTION: A PROCESS AND AGENTS FOR CELL PROLIFERATION DETECTION OR DIAGN
; TITLE OF INVENTION: AND A PROCESS AND AGENTS FOR INHIBITING CELL PROLIFERATION.
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Larson and Taylor
; STREET: 727 Twenty-Third Street, South
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 500 Kb storage
; COMPUTER: IBM PC/XT/AT or compatibles
; OPERATING SYSTEM: MS-DOS version 3.0 or above
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/650, 805
; FILING DATE: 06-FEB-1991
; APPLICATION NUMBER: FR9001596
; FILING DATE: 12-FEB-1990
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: Human cyclin A
; LOCATION: coding sequence from base 97 to base 1392,
; LOCATION: coding for a protein of 432 amino acids.

US-09-210-889-1
Query Match 7.7%; Score 125.6; DB 3; Length 1634;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;
QY 529 GAATGTCTCATGGATATTGACAGTGCAGACTCGGGGAACCCGTTGCTGCAACAGAAATAT 588
Db 571 GACATGTCATTTGATTAGAGATGAAAGCCAGTGTGTTAATGAAGTACAGACTAC 630
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAAGCCAGAT 648

Db 631 CATGAGGATATTCACATACCTTAGGGAATGGAGGTTAAATGTAAACCTAAAGTGGCT 690
QY 649 TACATGTCAGCAACAGAGCAATAAATCAAGATGAGAGCAATTTCTGATTTGACTGGCTG 708
Db 691 TACATGAAGAAACAGCCAGACATCACTAACAGTATGAGAGCTATCCTCGTGGACTGGTTA 750
QY 709 ATTGAGGTTCACTACAAGTTTGAAGTGTGATGATGAGAGGCTCTTTCTTTATGTTAAACATA 768
Db 751 GTTGAAGTAGGAGAGAGATATTAATCTACAGATGAGAGCCCTGCAATTTGGCTGTGAATAC 810
QY 769 ATAGATAGATTCTTGGAAGGAAGAGTGGTTCCAGAGAGAGAGCTACAAGTGTGGAGTTC 828
Db 811 ATTGATAGGTTCTGCTTCTTCCATGTGCTGAGTGGTGGAGGAAACCTTCAGCTTTGGGCACT 870
QY 829 ACAGCTATGCTGCTGCTGTTGTAATATGAGGAGGTATCTGTTCCAGTGTGTTGAGGACCTT 888
Db 871 GCTGCTATGCTGTTAGCTTCAAGTTTGAAGAAATATACCCCCAGAGAGTACAGAGTTT 930
QY 889 GTGCTGATATCTGACCGTGCCTACACAAAGGGGCAAAATTTTGAAGTGAAGAAAGTTGAT 948
Db 931 GTGTACATTACAGATGATACCTACACCAAGAAACAGTTTCTGAGAATGGAGCATCTAGTT 990
QY 949 CTGAACACGCTGAGTTCAACATGCTGTTCCAAACACCTTATGTTCTTCAATGA---AGAGG 1005
Db 991 TTGAAGTCTTACTTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
QY 1006 TTTCTGAAGCTGCAGATGCAAGTAAACAGCTTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 1065
Db 1051 TTTCTGATCAGCAGCCTGCAAACTGCAAAAGTTTGAAGTTTGAAGTTTGGGAGAA 1110
QY 1066 CTCGCTTGTGTAAGT---ACCAAGTGTGAATATCGGCTTTCGCAATCGGCTGCTGCT 1122
Db 1111 TTAAGTTTGAATAGATGCTGACCATCCTCAAGTATTTGCCATCAGTTATTTGCTGGAGCT 1170
QY 1123 GCGGTTTATCTGACAGTGTGCTATCA 1150
Db 1171 GCCTTTTATCTGACACTCTACACAGTCA 1198

RESULT 10

US-08-692-787-8
; Sequence 8, Application US/08692787
; Patent No. 5882864
; GENERAL INFORMATION:
; APPLICANT: An, Gang
; APPLICANT: O'Hara, S. Mark
; APPLICANT: Ralph, David
; APPLICANT: Veltri, Robert
; TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
; TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/692,787
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Corger, Timothy S.
; REGISTRATION NUMBER: 38,414
; REFERENCE/DOCKET NUMBER: UROC:012
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-692-787-8

Query Match 7.7%; Score 125.6; DB 2; Length 1649;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;

QY	529	GAATTGCTCATGATTTGACAGTGCACATCGGGAAACCGCTTCTGCTGCACAGATAT	588
DB	582	GACATGTCATTTGATTTAGAGATGAAGCCAGTGTAAATGAAGTACAGACTAC	641
QY	589	GTTAAAGAGCTTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTAAAGTGGT	701
DB	642	CATGAGATATTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTAAAGTGGT	701
QY	649	TACATGTCAGCCCAACAGATGAATCAAGATGAGAGCAATCTCAATGACTGGCTG	708
DB	702	TACATGAGAAACACCCAGACATCACTAACAGTATGAGAGTATCTCTGAGCTGTTA	761
QY	709	ATTGAGGTTCACTACAAGTTTGAAGTATGAGTGAAGAGCGCTTTCTTATGTTAAACATA	768
DB	762	GTTGAAGTAGGAGAGATATAAACTACAGAAATGAGACCTGCAATTTGGCTGTGAATAC	821
QY	769	ATAGATAGATTTTGGAAAGAGTGTTCACAGGAGAGAGCTACAACTGGTTGGAGTC	828
DB	822	ATTGATAGGTTCTGCTTCCATGTCTGAGTGTGAGGAGAAACTTCAGCTTGTGGGACT	881
QY	829	ACAGCTATCTGCTGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGACCTT	888
DB	882	GCTGCTATCTGTAGCTCAAAAGTTTGAAGAAATATACCCCCAGAGTAGCAGAGTTT	941
QY	889	GTGCTGATATCTGCGCTGCCTACACAAAGGGCAATTTAGAAATGGAAGTTGATT	948
DB	942	GTGTACATTTACAGATGATACCTTACACCAAGAACTCTGAGAAATGAGAGTATCT	1001
QY	949	CTGAACACGCTGCAGTTCAACATGCTGTTCACACACCTTATGTCTTCTCATGA---	1005
DB	1002	TTGAAAGTCTTACTTTTGCATTTAGCTGTCTCCACAGTAAATCAGTTCTTACCCATAC	1061
QY	1006	TTTCTGAAAGTGCAGATCCAGATGAACAGCTTTAGCTAGCTGCTCAATTTTTCATGCTGAG	1065
DB	1062	TTTCTGCACTCAGCAGCTGCAAACTGCAAAAGTTTGAAGTTTACAGTATGTTTGGAGAA	1121
QY	1066	CTCTGCTTGTGTAAGT---	1122

RESULT 11
US-09-097-199-8
Sequence 8, Application US/09097199
Patent No. 6218529
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: Ralph, David
APPLICANT: Velti, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-097-199-8

Query Match 7.7%; Score 125.6; DB 3; Length 1649;
Best Local Similarity 52.2%; Pred. No. 7.7e-25;
Matches 328; Conservative 0; Mismatches 294; Indels 6; Gaps 2;

QY	529	GAATTGCTCATGATTTGACAGTGCACATCGGGAAACCGCTTCTGCTGCACAGATAT	588
DB	582	GACATGTCATTTGATTTAGAGATGAAGCCAGTGTAAATGAAGTACAGACTAC	641
QY	589	GTTAAAGAGCTTTACACCTTTTACAGAAATGAGGCTTAAGTTGTTGAGCCAGAT	648
DB	642	CATGAGATATTTACACATACCTTAGGAAATGGAGTTAAATGTAACCTAAAGTGGT	701
QY	649	TACATGTCAGCCCAACAGATGAATCAAGATGAGAGCAATCTCAATGACTGGCTG	708
DB	702	TACATGAGAAACACCCAGACATCACTAACAGTATGAGAGTATCTCTGAGCTGTTA	761
QY	709	ATTGAGGTTCACTACAAGTTTGAAGTATGAGTGAAGAGCGCTTTCTTATGTTAAACATA	768
DB	762	GTTGAAGTAGGAGAGATATAAACTACAGAAATGAGACCTGCAATTTGGCTGTGAATAC	821
QY	769	ATAGATAGATTTTGGAAAGAGTGTTCACAGGAGAGAGCTACAACTGGTTGGAGTC	828
DB	822	ATTGATAGGTTCTGCTTCCATGTCTGAGTGTGAGGAGAAACTTCAGCTTGTGGGACT	881
QY	829	ACAGCTATCTGCTGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGACCTT	888
DB	882	GCTGCTATCTGTAGCTCAAAAGTTTGAAGAAATATACCCCCAGAGTAGCAGAGTTT	941
QY	889	GTGCTGATATCTGCGCTGCCTACACAAAGGGCAATTTAGAAATGGAAGTTGATT	948
DB	942	GTGTACATTTACAGATGATACCTTACACCAAGAACTCTGAGAAATGAGAGTATCT	1001
QY	949	CTGAACACGCTGCAGTTCAACATGCTGTTCACACACCTTATGTCTTCTCATGA---	1005
DB	1002	TTGAAAGTCTTACTTTTGCATTTAGCTGTCTCCACAGTAAATCAGTTCTTACCCATAC	1061
QY	1006	TTTCTGAAAGTGCAGATCCAGATGAACAGCTTTAGCTAGCTGCTCAATTTTTCATGCTGAG	1065
DB	1062	TTTCTGCACTCAGCAGCTGCAAACTGCAAAAGTTTGAAGTTTACAGTATGTTTGGAGAA	1121
QY	1066	CTCTGCTTGTGTAAGT---	1122

1122 TTAAGTTGATAGATGCTGACCATACCTCAAGTATTGCCATCATGTTATTGCTGGAGCT 1181
Db
1123 GCGGTTTATACTGCACAGTGTGTTATCA 1150
Qy
1182 GCCTTTCATTTAGCACTCTACAGTCA 1209
Db

RESULT 12

US-09-023-655-1268
Sequence 1268, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1268:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G30306
US-09-023-655-1268

Query Match	7.7%	Score 125.6	DB 4	Length 1649
Best Local Similarity	52.2%	Prod. No. 7.7e-25		
Matches 328	Conservative	0	Mismatches 294	Indels 6
			Gaps 2	
529	GAATGTCTCATGGNATTTGACATGTCAGACATCGGGAAACCCCTTGTCTGCAACAGAAATAT	588		
582	GACATGTCAATTTGATTAGAAGATGAAAAGCCAGTGAAGTTTAATGAAGTACCGACATC	641		
589	GTTAAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTTAAGAGTTGTGTAAAGCCAGAT	648		
642	CATGGGNATTTACACATACCTTAGGAAATGGAGTTTAATGTAAACCTTAAGTGGGT	701		
649	TACATGTCGCCCAACAAAGACATAAACTCAAGATGAGAGCAATTTCTGATTCAGTGGCTG	708		
702	TACATGAAGAAACAGCCAGACATCACTTAACAGTATCAGAGCTATCCTCGTGGATCGTTTA	761		

709 ATTGAGGTTCACTACAGTTTGAAGTGGATGAGACGCTCTTCTTATGCTAAACATA 768
762 GTTGAAGTAGGAGAGAAATATAAATACACAGAATGAGACCCCTGCATTGGCTGTGACTAC 821
769 ATAGATAGATTCTTTGGAAAAGGAGTGGTTCCAAGGAAGAAGCTACCACTGGTTGGAGTC 828
822 ATTGATAGGTTCCCTGCTTCTCCATGTCAGTGGCTGAGAGGAAAACCTCAGCTTGTGGCACT 881
829 ACAGCTATGCTGCTGCTGTTGTAATAATGAGGAGGTATCTGTTCCAGTTGTTGGAGACCTT 888
882 GCTGCTATGCTGTTAGCCCTCAAGTTTGAAGAAATATACCCCCACAGTAGCAGAGTTT 941
889 GTGCTGATATCTGACGCTGCTACAAAGGGGCAATTTTAGAAATGGAAGTTGATT 948
942 GTGTACATTACAGATGATACCTACCAAGAAACAGTTCTGAGAATGGAGCATCTAGTT 1001
949 CTGAACACGCTGCAGTTTCAACATGCTGTGTTCCAACACACCTTATGCTCTCATGA---AGAGG 1005
1002 TTGAAGTCTCTTACTTTTGACTTTAGCTGTGCTCCACAGATAATCAGTTTCTTACCCAATAC 1061
1006 TTTCTGAAGCTGCAGATGCAGATAAACAGCTTTGAGCTAGCGTCATTTTTCATGCTCGAG 1065
1062 TTTCTGCATCAGCAGCTGCAAACTGCCAAGTTGAAAGTTTGAAGTATGTTTGGAGAA 1121
1066 CTCGCTGTTGTAGAAAT---ACCAAGTGTGAATATACGGCTTCGCAATCGCTGCTGCTGCT 1122
1122 TTAAGTTTGTAGATGATGCTGACCCATACCTCAAGTATTTGCCATCAGTTTATGCTGGAGCT 1181
1123 CGCGCTTTATACGCAGCAGTGTGCTATCA 1150
1182 GCTTTTCATTAGCACTTACACAGTCA 1209

RESULT 13
US-08-463-090B-4
; Sequence 4, Application US/08463090B
; Patent No. 5801015
; GENERAL INFORMATION:
; APPLICANT: Cottarel, Guillaume
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Guilio
; TITLE OF INVENTION: Cell-Cycle Regulatory proteins from
; TITLE OF INVENTION: Human Pathogens, and Uses Related Thereto
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,090B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV032.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear

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MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 184...1659
US-08-463-090B-4

Query Match 7.3%; Score 119.6; DB 1; Length 1752;
Best Local Similarity 50.0%; Pred. No. 3.7e-23;
Matches 299; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

QY 540 GGAATTGACAGTCAGACTCGGGAAACCGCTTGGTGGCAACAGATATGTTAAAGAGCT 599
Db 750 GGAATTGACAGATGATGACGACCAATTAATGGTTAGTCAATATGTTAAACGAAT 809
QY 600 TTACACCTTTTACAGAGAAATGAGGCTTAAGAGTTGTGTAAGGCCAGATACATGTCAG 659
Db 810 ATTTTCGTACTATTACGATTTAGAAACACGAAATGTTACCTGATCCGCAATATCTTTTCA 869
QY 660 CCAACAGACATAAATCAAGATGAGAGCAATTTCTGATTTGATGCTGGCTGATGAGGTTCA 719
Db 870 ACAACATTTGTTAAACCAAGATGAGATCGATATGTTGTTGATTTGGCTTTGTTGAAATGCA 929
QY 720 CTACAGTTTGAATGATGAGAGAGCTCTTTCTTTATGTTAAACATAATAGATAGATT 779
Db 930 TTTAAATTTCAAGTTTATCTGATATCACITTTTTTGGCAGTCAATGTAATGATAGATT 989
QY 780 CTTGAAAAGGAAGTGGTTCCAGGAAGAGCTACAACTGGTTGGAGTCAACAGCTATGCT 839
Db 990 CATGCTCTTGAAGTGGTTCAATAGATAAATTAATTAATTTGGCTACAGCAGCTTTATT 1049
QY 840 GCTGCTTGAATATGAGGAGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATC 899
Db 1050 TACTGCTGCCAAAATGAAGAGTATTTCTCCCTGGTTAAATTAATGATATTTTCAAC 1109
QY 900 TGACCGTCCCTACACAAAGGGCAAAATTTAGAAATGAAAGTTGATTCTGAACACGCT 959
Db 1110 TGATGTTTCAATATCTCCAGAGAGTGGTACAGAGAGAAATACATGCTTACCAATCT 1169
QY 960 CGAGTTCAACATGCTGTTCCACACCTTATGTTCTCATGAGAGGTTCTGGAAGCTGC 1019
Db 1170 TAACCTTTGATTTGAATTAACCCCAATCCAAATGAAATTTCTTGAGAGAAATTTCTAAAGCTGA 1229
QY 1020 AGATCGATATAACAGCTTGAAGTACGCTGATCTTTTTCATGCTGGAGCTGCTGTTGATGA 1079
Db 1230 TGATTTGATGCTCAATCAAGACGCTAGGAAATATCTTTTGAATCACTATAGTTGA 1289
QY 1080 ATACCAATGCTGAATATATGCGCTTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 1137
Db 1290 TTACAAATTTATGCTATGAGACCATCTTTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 1347

RESULT 14
US-09-337-171-12
; Sequence 12, Application US/09337171
; Patent No. 6262249
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Giulia C
; TITLE OF INVENTION: PANCREATIC CANCER GENES
; FILE REFERENCE: 200130.454
; CURRENT APPLICATION NUMBER: US/09/337,171
; CURRENT FILING DATE: 1999-06-21
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-337-171-12

Query Match 6.8%; Score 111.6; DB 3; Length 826;
Best Local Similarity 55.0%; Pred. No. 4.1e-21;
Matches 219; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 727 TTTGAACTGATGATGAGACGCTCTTTCTTATGTTAAACATAATAGATAGATTCTTGGAA 786
Db 1 TTTAGGCTTCTGACGGGACTCTGTACATGTGCGTTCGCAATATGATCGATTTTACAG 60
QY 787 AAGGAAGTGGTTCCAGGAAGAGCTACAACTGGTTGGAGTCAAGCTATGCTGCTGCT 846
Db 61 GTTCAGCCAGTTTCCCGGAAGAAGCTTCAATTTAGTTGGGATTTACTGCTCTGCTGCGC 120
QY 847 TGTAAATATGAGGAGTATCTGTTCCAGTTTGGAGGACCTTGTGCTGATATCTGACCGT 906
Db 121 TCCAAGTATGAGGAGTATGTTTCTCCAAATATTTAGAGATTTGTTTACATCACAGACAA 180
QY 907 GCCTACACAAAAGGGCAAAATTTTAGAAATGGAAGTGAATTTCTGAAACACCGTGCAGTTTC 966
Db 181 GCTTATACCAAGTTCCCAATCCGAGAAATGGAATCTTAATTTTGAAGAAATCGAAATTT 240
QY 967 AACATGCTGTTCCAAACCTTATGCTTTTATGAGAGAGGTTCTTGAAGCTGCAGATGCA 1026
Db 241 GAGTTGGTTCGACCCCTTCCACTACACITTTTAAGGCGAGCATCAAAAGCCGGGAGGTT 300
QY 1027 GATAAACAGCTTGAAGTACGCTGATCTTTTCACTGTTGGAGCTGCTGTTGGTATGATACCAA 1086
Db 301 GATGTTGAACAGCACACTTTAGCCAAATTTTGAAGAGCTGACTCTCATCGACTATGAT 360
QY 1087 ATGCTGAATTAATCGGCTTTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1124
Db 361 ATGCTGAATTAATCATCTTCTTAAGGTAGCAGCAGCTGC 398

RESULT 15
US-09-773-459-12
; Sequence 12, Application US/09773459
; Patent No. 6664054
; GENERAL INFORMATION:
; APPLICANT: Kennedy, Giulia C
; TITLE OF INVENTION: PANCREATIC CANCER GENES
; FILE REFERENCE: 200130.454
; CURRENT APPLICATION NUMBER: US/09/773,459
; CURRENT FILING DATE: 2001-01-31
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-773-459-12

Query Match 6.8%; Score 111.6; DB 4; Length 826;
Best Local Similarity 55.0%; Pred. No. 4.1e-21;
Matches 219; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 727 TTTGAACTGATGATGAGACGCTCTTTCTTATGTTAAACATAATAGATAGATTCTTGGAA 786
Db 1 TTTAGGCTTCTGACGGGACTCTGTACATGTGCGTTCGCAATATGATCGATTTTACAG 60
QY 787 AAGGAAGTGGTTCCAGGAAGAGCTACAACTGGTTGGAGTCAAGCTATGCTGCTGCT 846
Db 61 GTTCAGCCAGTTTCCCGGAAGAAGCTTCAATTTAGTTGGGATTTACTGCTCTGCTGCGC 120
QY 847 TGTAAATATGAGGAGTATCTGTTCCAGTTTGGAGGACCTTGTGCTGATATCTGACCGT 906
Db 121 TCCAAGTATGAGGAGTATGTTTCTCCAAATATTTAGAGATTTGTTTACATCACAGACAA 180
QY 907 GCCTACACAAAAGGGCAAAATTTTAGAAATGGAAGTGAATTTCTGAAACACCGTGCAGTTTC 966
Db 181 GCTTATACCAAGTTCCCAATCCGAGAAATGGAATCTTAATTTTGAAGAAATCGAAATTT 240
QY 967 AACATGCTGTTCCAAACCTTATGCTTTTATGAGAGAGGTTCTTGAAGCTGCAGATGCA 1026
Db 241 GAGTTGGTTCGACCCCTTCCACTACACITTTTAAGGCGAGCATCAAAAGCCGGGAGGTT 300
```

Mon Mar 22 09:47:00 2004

Qy	1027	GATAAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAATACCAA	1086
Db	301	GATGTTGAACAGCACACTTTAGCCCAAGTATTTGATGGAGCTGACTCTCATCGACTATGAT	360
Qy	1087	ATGCTGAATTTATGGCCCTTCGCATCTGGCTGCTGCTGC	1124
Db	361	ATGGTGCATTATCATCCTTCTAAGGTAGCAGCAGCTGC	398

Search completed: March 20, 2004, 23:05:47
Job time : 134 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 20, 2004, 19:50:55 ; Search time 585 Seconds
(without alignments)
10344.983 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1636
Sequence: 1 tcaagggtctctccgctcg.....aaaaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubna/FCN_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubna/PTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq:
17: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq:
18: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1634	98.9	1636	10	US-09-496-444-1
2	1610	98.4	1699	15	US-10-310-154-50
3	702.2	42.9	1611	15	US-10-310-154-46
4	400.6	24.5	1793	15	US-10-310-154-44
5	388.8	23.8	1896	12	US-10-424-599-4753
6	355.4	21.7	1750	15	US-10-310-154-61
7	342.4	20.9	1281	15	US-10-260-238-497
8	243.8	14.9	1751	15	US-10-310-154-51
9	228.6	14.0	1141	12	US-10-424-599-11853
10	228.6	14.0	1384	15	US-10-260-238-1251
11	220.6	13.5	1344	12	US-10-424-599-103481
12	215.4	13.2	1816	12	US-10-424-599-118855
13	214.6	13.1	1338	9	US-09-938-842A-789
14	214.6	13.1	1338	11	US-09-938-842A-789
15	212.8	13.0	1850	15	US-10-310-154-52

16	212.2	13.0	715	12	US-10-424-599-24154
17	211.2	12.9	1086	12	US-10-425-114-17906
18	195.6	12.0	605	12	US-10-424-599-98711
19	173.2	10.6	1879	15	US-10-310-154-56
20	161.4	9.9	1553	9	US-09-925-301-305
21	157	9.6	1197	10	US-09-994-412-2
22	155.4	9.5	1452	9	US-09-954-456-695
23	155.4	9.5	1452	9	US-09-954-456-1133
24	155.4	9.5	1452	9	US-09-880-107-2308
25	155.4	9.5	1452	9	US-09-967-768A-145
26	155.4	9.5	1452	9	US-09-954-531-147
27	155.4	9.5	1452	9	US-09-292-758-27
28	155.4	9.5	1452	10	US-09-873-367C-1008
29	155.4	9.5	1452	14	US-10-171-581-136
30	155.4	9.5	1570	13	US-10-098-841-236
31	152	9.3	1278	14	US-10-128-714-2013
32	152	9.3	1347	14	US-10-128-714-1013
33	152	9.3	1464	14	US-10-128-714-7013
34	152	9.3	1577	14	US-10-128-714-6013
35	152	9.3	3347	14	US-10-128-714-13
36	152	9.3	3577	14	US-10-128-714-5013
37	149.2	9.1	873	12	US-10-424-599-52554
38	139.6	8.5	1905	12	US-10-425-114-13500
39	134.2	8.2	1539	15	US-10-369-493-27403
40	129.4	7.9	1247	15	US-10-085-198-109
41	127.2	7.8	1446	15	US-10-369-493-26031
42	127.2	7.8	1446	15	US-10-369-493-26040
43	125.6	7.7	1649	10	US-09-974-546-8
44	125.6	7.7	2504	13	US-10-108-605-246
45	125.6	7.7	3740	9	US-09-925-300-345

ALIGNMENTS

RESULT 1
US-09-496-444-1
; Sequence 1, Application US/09496444
; Publication No. US20030041343A1
; GENERAL INFORMATION:
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm William J.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Bailey, Matthew A.
; TITLE OF INVENTION: Cell Cycle Polynucleotide, Polypeptide,
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1109
; CURRENT APPLICATION NUMBER: US/09/496,444
; CURRENT FILING DATE: 2000-02-02
; EARLIER APPLICATION NUMBER: US 60/119,857
; EARLIER FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: US 60/101,551
; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: US 09/398,858
; EARLIER FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: US 09/257,131
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)...(1381)
; NAME/KEY: misc feature
; LOCATION: (1)...(1636)
; OTHER INFORMATION: n = A,T,C or G
US-09-496-444-1

Query Match 99.9%; Score 1634; DB 10; Length 1636;
Best Local Similarity 100.0%; Pred. No. 0;

	Matches	1636;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TCACGGGGTCTCTCCGTTCGGTAAGGCAACCGCCGACGCTCTCGGTGATCAACAGCGCG	60							
Db	1	TCACGGGGTCTCTCCGTTCGGTAAGGCAACCGCCGACGCTCTCGGTGATCAACAGCGCG	60							
Qy	61	GCGCATCCGTCCTTTCCCTCTCTCTCGGGGTCCGGCTTTGGGGATCATGCGCGCGCG	120							
Db	61	GCGCATCCGTCCTTTCCCTCTCTCTCGGGGTCCGGCTTTGGGGATCATGCGCGCGCG	120							
Qy	121	GCGGCTGAACGAAACAGAGAACCGCGGCGAGGGAAGCCCGCCAGGCGTTCGAGACATG	180							
Db	121	GCGGCTGAACGAAACAGAGAACCGCGGCGAGGGAAGCCCGCCAGGCGTTCGAGACATG	180							
Qy	181	GCGAGCGGCGCGCGCTCACGACATCAAGAACTCTCTGGGGCTCCCGCGTACCCCTAC	240							
Db	181	GCGAGCGGCGCGCGCTCACGACATCAAGAACTCTCTGGGGCTCCCGCGTACCCCTAC	240							
Qy	241	GCGGTGCCAAGAGCCCATCTGTCAGAGACGAAAGGACGAAAGCAGCAGCAGGTTG	300							
Db	241	GCGGTGCCAAGAGCCCATCTGTCAGAGAGCAAAAGGACGAAAGCAGCAGGTTG	300							
Qy	301	GCAAGCAGCGCGCCATGACAGGAAATTCGCGCCTCTTGGCGAGCAGGCGCAACT	360							
Db	301	GCAAGCAGCGCGCCATGACAGGAAATTCGCGCCTCTTGGCGAGCAGGCGCAACT	360							
Qy	361	GAATGTCAGCGCATCTGATGATCCAGAACCCGAGTTTGTCAAACAGAGGAATCAGTA	420							
Db	361	GAATGTCAGCGCATCTGATGATCCAGAACCCGAGTTTGTCAAACAGAGGAATCAGTA	420							
Qy	421	GGGGATGGCACCGTTGATATTGACGTGGAACTCTACGAGCTGTCGACCGTAGTGATG	480							
Db	421	GGCGATGGCACCGTTGATATTGACGTGGAACTCTACGAGCTGTCGACCGTAGTGATG	480							
Qy	481	GACATCCAGATGGGTGGCAGAGAACAGGACATATGAAACGAATGAATTCCTCATG	540							
Db	481	GACATCCAGATGGGTGGCAGAGAACAGGACATATGAAACGAATGAATTCCTCATG	540							
Qy	541	GATATTGACAGTGCAGACTCGGGGAAACCCGCTTGCTGCAACAGAAATATGTTAAAGAGTT	600							
Db	541	GATATTGACAGTGCAGACTCGGGGAAACCCGCTTGCTGCAACAGAAATATGTTAAAGAGTT	600							
Qy	601	TACACCTTTTACAGAGAAATGAGCTTAAGATTGTTGTAAGGCCAGATTACATGTCACG	660							
Db	601	TACACCTTTTACAGAGAAATGAGCTTAAGATTGTTGTAAGGCCAGATTACATGTCACG	660							
Qy	661	CAACAAGACATAAACTCAAAGATGAGAGCAATTCGATTGACTGGCTGATTGAGGTTTCA	720							
Db	661	CAACAAGACATAAACTCAAAGATGAGAGCAATTCGATTGACTGGCTGATTGAGGTTTCA	720							
Qy	721	TACAAGTTTGAACGTGAGTACAGCCCTCTTCTTATGTTGTTAAACATAATAGATGATTC	780							
Db	721	TACAAGTTTGAACGTGAGTACAGCCCTCTTCTTATGTTGTTAAACATAATAGATGATTC	780							
Qy	781	TTGGAAAAGGAAAGTGGTTTCCAAGGAAGAAGCTACAACTGGTTGGAGTCAAGCTATGCTG	840							
Db	781	TTGGAAAAGGAAAGTGGTTTCCAAGGAAGAAGCTACAACTGGTTGGAGTCAAGCTATGCTG	840							
Qy	841	CTCGCTTTGAATATGAGGAGTATCTGTTCCAGTCTGTGAGGACCTTTGCTGCTGATATCT	900							
Db	841	CTCGCTTTGAATATGAGGAGTATCTGTTCCAGTCTGTGAGGACCTTTGCTGCTGATATCT	900							
Qy	901	GACCGTGCTTACAAAAAGGCGCAATTTTAGAAATGGAAGTTGATCTTGAACACCGCTG	960							
Db	901	GACCGTGCTTACAAAAAGGCGCAATTTTAGAAATGGAAGTTGATCTTGAACACCGCTG	960							
Qy	961	CAGTTTCAATGTCGTTTCCAACACCTTATGCTTCTATGAAAGAGGTTTCTGAAAGCTGCA	1020							
Db	961	CAGTTTCAATGTCGTTTCCAACACCTTATGCTTCTATGAAAGAGGTTTCTGAAAGCTGCA	1020							
Qy	1021	GATGCAGATAAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAA	1080							
Db	1021	GATGCAGATAAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAA	1080							

RESULT 2

US-10-310-154-50

: sequence 50. Application US/10310154

Publication No. US20030233670A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

APPLICANT: CHOMET, PAUL S.

APPLICANT: Adams, Thomas H

APPLICANT: ADAMS, THOMAS H.
APPLICANT: BUFF, THOMAS G.

APPLICANT: RULL, Thomas G.
APPLICANT: Agarwal, Ameeta K.

APPLICANT: Agalwal, Ananda K.
APPLICANT: Ahrens, Jeffrey E.

APPLICANT: Ball, James A.

APPLICANT: BARI, James A.
APPLICANT: BARI, G.

APPLICANT: BELL, G.
APPLICANT: BELL, ERIN

APPLICANT: BEIL, EITH
APPLICANT: BODDUNALLI, RAGHAV

APPLICANT: BOGDURATLI, KAGHAN
APPLICANT: DEIKMAN, JILL

APPLICANT: DENA MOLIAN
APPLICANT: DENA MOLIAN

APPLICANT: Deng, Molian
APPLICANT: Deng, Jinzhu

APPLICANT: DOUG, BRUNO
APPLICANT: DUFF, STEPHEN M.

APPLICANT: DUFF, Stephen M.
APPLICANT: Galligan, Meghan M.

APPLICANT: Hinchey, Brenda S

APPLICANT: HINCNEY, Brenda S.
APPLICANT: Huang, Shihshieh

APPLICANT: Huang, Shihshien
APPLICANT: Johnson, G. Richard

APPLICANT: JUNG VINCENT

APPLICANT: Kretzmer, Vincent
APPLICANT: Kretzmer, Keith A

APPLICANT: KIEZMER, KATHA A

APPLICANT: LACCETTI, LUCILLE
APPLICANT: LAI, CHAO-CHANG
APPLICANT:

APPLICANT: Lai, Chao-Qiang
APPLICANT: Lee, Gary

APPLICANT: Lee, Gary
APPLICANT: Tice, V

APPLICANT: Lin, Jie-Yi
APPLICANT: Lin, Jie-Yi
APPLICANT: Lin, Jie-Yi

APPLICANT: Liu, Jingdong
APPLICANT: Liu, Ping

QY	1128	TTATATCGCACACGTGCTACTCAATCGTTCGCACGACCTGACGACCAAGGCTCGCGAGTCTCA	1187
Db	1075	TTACACAGCAAAATGTGCTCTCACTCGTTCGCACAGCTGGACAAGACCTGCGAATAC	1134
QY	1188	TACGAGATACATPACGACCAATCTCTGGAGTGTCTGAGATGATGTGTAGATTTTCAACA	1247
Db	1135	TAGTAGATATACCGAGAGACGCTCTTAGTGTCTTAGATGATGTGTAGATTTCCACCA	1194
QY	1248	GAAGGCTGGAAACCAATGTAAGCTCACTGCGCTGCACAGGAAGTACAGTACCTACAGTTTCGG	1307
Db	1195	GAAGGGGGGAGCAGCGCAAGCTCAACCGCGCTGCACCGGAATAACAGTACGTTTCAAGTTTGG	1254
QY	1308	TTGCGTGGCCAAAGATTTTGGCTCGGCAGTTTCTGCTCGAGTCGGGAG--GGACACCGCCCT	1365
Db	1255	GTGTGACGCCAAAACGAGAGCTGTCTCTCTTCTGTTGAGTTCAGGACGAGAGGTTACAA	1314
QY	1366	CTTTCAGGTCGAACTAGTTGAATPCGACCTATTCAACTGGGTGGATTTTTTAAAGTT	1422
Db	1315	CTTTCAGAACGAGCTGTTGAATGAATCTATTCCCTCGATAGATTTTTTAACTT	1371

RESULT 4

US-10-310-154-44
; Sequence 44, Application US/10310154
; Publication No. US20030233670A1

; PUBLICATION NO: 0320
: GENERAL INFORMATION:

1	APPLICANT: Edgerton, Michael D
2	APPLICANT: Chomet, Paul S.
3	APPLICANT: Adams, Thomas H.
4	APPLICANT: Ruff, Thomas G.
5	APPLICANT: Agarwal, Aneseta K.
6	APPLICANT: Ahrens, Jeffrey E.
7	APPLICANT: Ball, James A.
8	APPLICANT: Banu, G.
9	APPLICANT: Bell, Erin
10	APPLICANT: Boddepalli, Raghava
11	APPLICANT: Deikman, Jill
12	APPLICANT: Deng, Molian
13	APPLICANT: Dong, Jinzhuo
14	APPLICANT: Duff, Stephen M.
15	APPLICANT: Galligan, Meghan M.
16	APPLICANT: Hinchey, Brenda S.
17	APPLICANT: Huang, Shihshieh
18	APPLICANT: Johnson, G. Richard
19	APPLICANT: Jung, Vincent
20	APPLICANT: Kretzmer, Keith A.
21	APPLICANT: Laccetti, Lucille B.
22	APPLICANT: Lai, Chao-Qiang
23	APPLICANT: Lee, Gary
24	APPLICANT: Lin, Jie-Yi
25	APPLICANT: Liu, Jingdong
26	APPLICANT: Lu, Bin
27	APPLICANT: Luethy, Michael M.
28	APPLICANT: Lund, Adrian
29	APPLICANT: Madson, Linda L.
30	APPLICANT: Malloy, Kathleen A.
31	APPLICANT: McKiel, Christine L.
32	APPLICANT: Miller, Philip W.
33	APPLICANT: Padmavathi, Manchikanti
34	APPLICANT: Parnelli, Laurence D.
35	APPLICANT: Startt, William G.
36	APPLICANT: Tennesen, Dan
37	APPLICANT: Vidya, K.R.
38	APPLICANT: Wang, Haiyun
39	APPLICANT: Xin, Zhangguo
40	APPLICANT: Xu, Nanfei
41	APPLICANT: Yang, Chunzhi
42	APPLICANT: Zeng, Xiaoping
43	APPLICANT: Zhang, Qiang
44	APPLICANT: Zhao, Yajuan
45	APPLICANT: Zhou, Li
46	FILE OF INVENTION: Gene Sequences
47	FILE REFERENCE: 38-15(52796)B

```

; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 44
; LENGTH: 1793
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1407)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1793)
; OTHER INFORMATION: unsure at all n locations
US-10-310-154-44

Query Match 24.5%; Score 400.6; DB 15; Length 1793;
Best Local Similarity 68.5%; Pred. No. 3.2e+109;
Matches 553; Conservative 0; Mismatches 254; Indels 0; Gaps 0;

QY 541 GATATTGACAGTGCAGACTCGGGGAACCCGCTTGCTGCAACAGAAATATGTTAAGAGCTT 600
DB 586 GATATTGACAGCTGTGATGCCAATAACTCCCTTGCAGTAGTTGAATATGTTGATGAATT 645
QY 601 TACACCTTTTACAGAGAAATAGGCTTAAGAGTTGTGTAAGGCCAGATTACATGTCACGC 660
DB 646 TACAGCTTCTACAGGAGGAGTGAAGGCTTTGAGCTGTCTCTCCTAATTACATGTTGAGC. 705
QY 661 CAACAAGACATAAACTCAAAGATGAGAGCAAAATCTCAATGCATCTGGCTGATGAGGTTCC 720
DB 706 CAAATGACATAAATGAGAAGATGCGCGCAITCTCATCGATTGGCTGATAGAGGTGCAT 765
QY 721 TACAGTTTGAATGATGATGAGAGCGCTTCTTTATGGTAAACATAATAGATAGATTCT 780
DB 766 TACAGTTGAGCTATTGATGAGAGCCCTCTCCCTACTGTGAATATCATAGACCCGATTC 825
QY 781 TTGCGAAAGGAAGTGTTCAGAGGAAGAGCTACAACCTGGTTGGAGTTCAGAGCTATGCTG 840
DB 826 TTGGCTCGCGAAATGTGGTGCGAAGAGCTTCAGTTGGTTGGCGTGACTGCCATGCTG 885
QY 841 CTGCTGTGTAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCT 900
DB 886 CTCGCTGCAAGTATGAAGAAGTGAGCGTTCTCTGTAGTGGAGATCTTATCCTAACTGCG 945
QY 901 GACCGTGCCTACACAAAAGGCGAAATTTTGAATAATGGAAAAGTTGATTTCTGAAACAGCTG 960
DB 946 GACGCGCCTACACAAGAACAGATATCTCGAAATGGAGAGGATGATTTGAAACACTCTTT 1005
QY 961 CAGTTTCAATGCTGTTTCCAAACACCTTATGCTTTTATGAGAGGTTTCTTCAAGGCTGCA 1020
DB 1006 CAGTTTGATATGTCAGTTTCCAACTCCATACCTGTTTCATGAGAGGTTTCTTCAAGGCTGCA 1065
QY 1021 GATGCAGATAAAGCAGCTTGAGCTAGCGTCAATTTTTTCATGCTGGAGCTCTCTCTGGTAGAA 1080
DB 1066 CAATCTGACAAGAAGCTTTGAGCTCATGCTTTTCTTCATAATTGAGCTGAGCCTTGTGAG 1125
QY 1081 TACCAATGCTGAATTAATCGGCGCTTGCCATCTGCTGCTGGGTTTATCTGACACAG 1140
DB 1126 TATGAGATGCTCAAAATCCAGCGCGTCAATGCTGCGGCTGCTGCCATCTACATGCTCTCAG 1185
QY 1141 TGTGCTATCAATCGTTGCCAGCACTGCACAAAGGTCTGCGAGTCTCATAGCAGATACACT 1200
DB 1186 TGCACCAATTAATGGGTTCAAGTCTCGAACAATAATGCTGTGAGCTGCATACAAATACTCT 1245
QY 1201 AGCGACCACTCTCGGAGTCTCGAGGATGATGCTAGATTTTCCACAGAGGCTTGGAAAC 1260
DB 1246 GAGAAACAGCTGATGAGTGCTCCAGATGATGGTTGAGCTTCCACCAAAAGACGAGACAT 1305
QY 1261 AGTAAGCTCACTGGCGTGCAAGAGAGTACAGTACCTTACAGTTTCGGTTCGGTGCCAAAG 1320

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FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 61
LENGTH: 1750
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (114)...(1385)
OTHER INFORMATION:
US-10-310-154-61

Query Match 21.7%; Score 355.4; DB 15; Length 1750;
Best Local Similarity 54.8%; Pred. No. 1.3e-95;
Matches 527; Conservative 0; Mismatches 286; Indels 0; Gaps 0;

QY 541 GATATTGACAGTGCAGACTCGGGAAACCGCTTGTGCTGCAACAGATATGTTAAAGAGCTT 600
DB 576 GATATTGACAGTGCAGAAATTCCTGGCTGGCTGACTATGATGAAT 635
QY 601 TACACCTTTTACAGAGAAATAGGCTAAGAGTTGTGTAAGGCCAGATTACATGTCACG 660
DB 636 TACAGATTTTACAGGAAACTGAGGGTGCAAGCTCGCTCCCTACAAATATATGTCAAGC 695
QY 661 CAACAGACATAACTCAAGATGAGCAATTCGTATGACTGGCTGATGAGTTTAC 720
DB 696 CAACTGATATAATGAGAAGATGCGTGCCATCTTAATTGACTGGCTCATAGAGTAC 755
QY 721 TACAAAGTTGAAGTATGATGATGAGAGCTCTTCTTATGTTAAACATATAGATATTC 780
DB 756 TACAACTAGAGCTGTGGAGGAGACCTTTTCTTCAACGCTGAACATCATAGAGATTC 815
QY 781 TTGAAAAGGAAGTGGTCCAGAGGAAGAGCTTACAACTGTTGGAGTCACAGCTATGCTG 840
DB 816 TTGGCAGCTGAAATGTGGTGGGAAAGAGCTTCAAGTGTAGTGGTGAATGCTATGTTG 875
QY 841 CTCGGTTGTAATATGAGGAGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCT 900
DB 876 CTCGGGTGCAATATGAGAAGTGAAGCTGACCTGTGTCGAGGATCTGATCTGATCGT 935
QY 901 GACCGTCCCTACAAAAGGGCAATTTTAGAAATGGAAGTTGATTCGAAACAGCTG 960
DB 936 GATCGTCATACACAGGGCTGACATCTTGAGATGGAGAGGATAGTGAACACACTT 995
QY 961 CAGTTCAACATGTCCTTCCAAACACCTTATGCTTTCATGAAGAGGTTTCTGAAGCTGCA 1020
DB 996 AATTTCAATATGTCGGTCCGACTCCATCTGTTTCATGAGAGAGTTTCTAAGGACGA 1055
QY 1021 GATGCAGATTAACAGCTTGAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1056 CAATCAGAGAAGAGCTGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1115
QY 1081 TACCAATGCTGAATATATCGGCTTCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1116 TATGAGATGCTCCAGTCTGCTCCGCTTATGCTAGCAGCGCTGCCATCTACACCGCTCAA 1175
QY 1141 TGTGCTATCAATGCTTCCAGCACTGGCAAAAGGCTTCTGAGTCTCATAGCAGATACACT 1200
DB 1176 TGCACCATAAATGGGTTCAAGTCTTGGAAACAAATGCTGTGAACCTGCACAAAGATATCA 1235
QY 1201 AGGACCACTCTGAGTGTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1236 GAAGACATCTAATGTTTGTCTAGGATGATGATGATGATGATGATGATGATGATGATGAT 1295
QY 1261 AGTAAGCTCACTGGCTGCACAGAGAGTACAGTACCTTCAAGTTCGGTTGGTGGCCCAAG 1320
DB 1296 GGGAAACTTACAGGGTCCATAGAAAGTACACACTTCTAGATATAGTATGCTGCTGAA 1355
QY 1321 ATTTGCTGGGAGTTCCTGCTGGAGTCGGGA 1353

DB 1356 TCGGAACCCGCAACTTTCTTGTGGATGCTCGA 1388

RESULT 7

US-10-260-238-497
Sequence 497, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyuki
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 497
LENGTH: 1281
TYPE: DNA
ORGANISM: Oryza sativa
US-10-260-238-497

Query Match 20.9%; Score 342.4; DB 15; Length 1281;
Best Local Similarity 67.8%; Pred. No. 8.7e-92;
Matches 556; Conservative 0; Mismatches 251; Indels 13; Gaps 5;

QY 541 GATATTGACAGTGCAGACTCGGGAAACCGCTTGTGCTGCAACAGATATGTTAAAGAGCTT 600
DB 447 GATATTGACAGCTGTGATGCAATAACTCCCTTGCAGTAGTTGAATATGTTGATGAAT 506
QY 601 TACACCTTTTACAGAGAAATG---AGGCTAAGAGTTGTGTAAGGCCAGATTACATGTC 657
DB 507 TACAGCTTCTACAGGAGGAGTGAGCAGGGTTTGAGCTGTCTCTCTCTCTCTCTCTCT 566
QY 658 AGCCAAACAGACATAAATCCAAAGATGAGAGCAATTCGATTGACTGGCTGAT--TGAGG 715
DB 567 AGCCAAATGACATAATAGAGAGATCGCGGCAATTCATCGATTGGCTGATAGAGG 626
QY 716 TTCACTACAAGTTGAAGTATGATGATGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 775
DB 627 TGCATTACAAGTTAGAGCTATTGATGAGAGACCTCTCTCTCTCTCTCTCTCTCTCTCT 686
QY 776 GATTCTGGAAGAGGAGTGGTTCCAAAGAGAGCTCAACCTGGTTGGAGTCACAGCTA 835
DB 687 GATTCTTGGCTCCGAAATGTGGTGGAAAGAGCTTCAGTTGGTTGGCTGACTGCCA 746
QY 836 TGTCTGCTGCTGTTGTAATATGAGGAGGATCTCTCTCCAGTTGTGAGGACCTTGTGCTGA 895
DB 747 TGTCTGCTGCTGCAAGTATGAAGAGTGAAGCTTCTCTGTAGTGGAGGATCTTATCTTAA 806
QY 896 TAICTGACCTGCTTACACAAAGGGCAATTTTGAAT--GAAAAGTTGATTCCTCAAC 954
DB 807 TCTGCGACCGCTTACACAAAGAGATATCTCGAAATGGAGAGGATGATTTGTAAC 866
QY 955 ACGCTGAGTTCAACATGCTGTTCCAAACACCTTATGTTCTTCAAGAGGTTTCTGAA 1014
DB 867 ACTCTTCAGTTGATATGTCAGTTCCAACTCCATACTGTTTCAATGAGAAGTTCTCCTCAAG 956

QY 1015 GCTGAGATGACAT-----AAACAGCTTGTAGCTAGCTATTTTTCATGCTGAGCTC 1068
Db 927 GCTGCAATCTGACAGAAACAGCTTGTAGCTATGCTTTCTTCTATATAATGAGCTG 986
QY 1069 TGTGTTGTAAGAACCAATGCTGAATATATGCGCTTGGCATCTGCTGCTGCTGCTGCTG 1128
Db 987 AGCTTGTGAGTATGAGATGCTCAATTCACGCTCAATGCTGCGGCTGCTGCTGCTG 1046
QY 1129 TATATGACAGTGTGCTATCAATGCTGCGCATCTGACATGGAACAAAGCTTGGAGTCTCAT 1188
Db 1047 TACATGCTCAGTGACCAATTAATGCTTCAAGTCTGGAACAAATGCTGCTGAGCTGCAT 1106
QY 1189 AGCAGATACACTAGCAGCAACCTCT--GGAGTCTGAGATGATGCTAGATTTTCAACA 1247
Db 1107 ACATAATCTCTGAGACAGCTGATGAGAGTCTCTCAAGATGATGCTGAGCTCAACA 1166
QY 1248 GAAGGCTGGAACCAAGTAACTGCTGCGTGCAGAGAGTACAGTACCTCAAGTTCGG 1307
Db 1167 AAAAGCAGGACATGGGAAGCTTACTGAGTTCTATAGAAAGTACAGCACATTTAGGTATGG 1226
QY 1308 TTGCTGCGCAAGATTTTGGCTGCGCAGTTTCTGCTGCTGGAG 1347
Db 1227 TTGCGCCGCAAAATCGAGCCCGCTTCTTCTGCTCAAG 1266

RESULT 8

US-10-310-154-51
Sequence 51, Application US/10310154
Publication No. US20030233670A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H.
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupallli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deng, Molian
APPLICANT: Dong, Jinchuo
APPLICANT: Duff, Stephen M.
APPLICANT: Galligan, Meghan M.
APPLICANT: Hinchey, Brenda S.
APPLICANT: Huang, Shihshieh
APPLICANT: Johnson, G. Richard
APPLICANT: Jung, Vincent
APPLICANT: Kretzmer, Keith A.
APPLICANT: Laccetti, Lucille B.
APPLICANT: Lai, Chao-Qiang
APPLICANT: Lee, Gary
APPLICANT: Lin, Jie-Yi
APPLICANT: Liu, Jingdong
APPLICANT: Lu, Bin
APPLICANT: Luerhy, Michael M.
APPLICANT: Lund, Adrian
APPLICANT: Madson, Linda L.
APPLICANT: Malloy, Kathleen A.
APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang

APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 51
LENGTH: 1751
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (82)..(1518)
OTHER INFORMATION:
US-10-310-154-51

Query Match 14.9%; Score 243.8; DB 15; Length 1751;
Best Local Similarity 56.0%; Pred. No. 5.5e-62;
Matches 461; Conservative 0; Mismatches 362; Indels 0; Gaps 0;
QY 541 GATATTGACAGTGCAGACTCGGGAACCCGCTTGTCTCAACAGATATGTTAAAGAGCTT 600
Db 709 GACATTGATGCACCTGATTTCTTGAATGAGTGGCAGTCTGTTGAATATGTTGAGACATT 768
QY 601 TACACCTTTTACAGAGAAATGAGGCTTAAGAGTTGTCTAAAGGCCAGATTTACATGCCAGC 660
Db 769 TACAGATTCTACAAGAGACACTGAGGGCACCTGCTCCTCTCAGCAGCTACATGAGTCA 828
QY 661 CAACAAGACATAAATCAAGATGAGAGCAATTTCTGATTGACTGGCTGATTGAGTTTAC 720
Db 829 CAGGCTGAATCAGTGAAGAGAAATGAGAGCTATCTCTTATTGACTGGATATGAGAGGTACAG 888
QY 721 TACAAGTTTGAACCTGATGATGAGAGTACAGAGCTCTTTCTTATGTTAAACATAATAGATATTC 780
Db 889 TACAGGCTTACTCTAATGCCAGAGACACTTTACTTTCGCTCTACATCATGACCACTAC 948
QY 781 TTGGAAGAGAGTGGTTTCCAGAGAGAGTACAACTGTTGAGTGCAGAGTATGCTG 840
Db 949 TTATCTATGAGAGTGTACCAAGAAAGGAGCTACAGCTCTGCGGCAATGAGTGGCATGCTG 1008
QY 841 CTCGCTTGTAAATATGAGGAGTATCTGTTCCAGTGTGTTGAGGACCTTGTCTGATATCT 900
Db 1009 ATAGCAAGCAAGTACGAGAGATATGGCTCCACTGTTAGGACTTGTATGCTTATGT 1068
QY 901 GACCGTGCTACAAAAAGGGCAATTTTGAAGATGAAAAAGTTGATTCTGAACACGCTG 960
Db 1069 GACAACGCATTTTACCAGAGAGCCAGATTCTGACCAAGGAAAAAGGCCATCTCGACATGCTC 1128
QY 961 CAGTTTCAACATGCTGTTTCCAAACACCTTATGTTCTTATGAAGAGAGTTTCTGAAAGCTGCA 1020
Db 1129 CATTTGAACTGACGGTTTCCAAACATGTAATGTAATGTTTATGTTAGTACCTGAAAGCCGCA 1188
QY 1021 GATGAGATAAACAGCTTGTAGCTAGCTGCTCATTTTTCATGCTGAGAGTCTGCTTGGTGA 1080
Db 1189 ATGTGTGACGAGAGCTTGAAGACATGATCTTCTACTCCGAGCTGGCATTTGCTCCAG 1248
QY 1081 TACCAATGCTGAATTTATCGGCTTTCGCATCTGGCTGCTGCTGCTGCTGCTTATCTGACAG 1140
Db 1249 TACGGATGCTGGTTTATCTCTCATCGGTGACCGGCGCTGCGCTGCTGCTGCTGCTGCTG 1308
QY 1141 TGTGCTATCAATCGTTTGGCAGCAGTGGCAAGAGTCTCGAGTCTCTCATGAGAGATACACT 1200
Db 1309 TCTACACTTGGGATGAATCCACAGTGGAGTATTTCTGGAACATCACACTGGCTAGCT 1368
QY 1201 AGCGACCAACTCTCGAGTGTCTGAGGATGATGTTTCTCCAGAGAGCTGGAGAC 1260
Db 1369 GAGCCACAGTTTACTGAGCTGGCTAGGCGGTGATCAGCTTCCATGCCCTGCTCCGAA 1428
QY 1261 AGTAAAGTCACTGGGCTGCACAGAGAGTACAGTACTCAAGTTTCGGTTGGCTGGCCCAAG 1320

Db 1429 AGCAAGCAAAAGGGGTGTACAGGAAGTACTCCAAAGCCAAAGCTCGGCTCGTGGCGTT 1488
QY 1321 ATTTTGGCTGGCGAGTCTCTGCTGAGTCCGGAGGACACCGC 1363
Db 1489 CAATCCCTGACAAAGAGCTGTGTGACAGTTGAGGCTCGCTGC 1531

RESULT 9

US-10-424-599-118853
; Sequence 118853, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 118853
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1141)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_78333C.1
US-10-424-599-118853

Query Match 14.0%; Score 228.6; DB 12; Length 1141;
Best Local Similarity 56.7%; Pred. No. 1.5e-57;
Matches 442; Conservative 0; Mismatches 334; Indels 3; Gaps 1;

QY 568 CGCTTGTGTGCAACAGATATGTTAAAGAGCTTTTACACCTTTTACAGAGAAATGAGCT 627
Db 30 CGCTTGTGTGTGGAGTCAATGATGACATTTTACAGTTTCTACAACTTTGTTGAAAC 89
QY 628 AAGAGTTGTGTAAAGCCAGATTACATGTCACGCAACAAAGACATAAACTCAAGATGAGA 687
Db 90 GAGA---GCCACCCACGACTACATTGATTCACACCTGAATTAATGAGAGATGAGA 146
QY 688 GCAATCTGATGACTGGCTGATGAGGTTCACTACAAAGTTTGAAGTGTGATGATGAGAGC 747
Db 147 GCTATCTGTTGATGTTGGCTGATGAGAGCTTACACCAAGTTTGAACCTTCTCTAGAGACC 206
QY 748 CTCCTTCTTATGGTAAACATAATAGATAGATTCTTGGAAAAGGAAGTGGTTCCAAAGGAAG 807
Db 207 CTTTACCTGACCATCAACATAATGATCGGTTTGTAGCAGTTAAGACAGTTTCCAAAGGAGG 266
QY 808 AAGCTAACACTGGTTGGAGTCACAGCTATGCTGCTGCTTGTGCTTAATATGAGAGGATATCT 867
Db 267 GAACCTGCAATTGGTTGGCATCAGTGCCTATGCTGATGGCATCCAAATATGAGAAATCTGG 326
QY 868 GTTCCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACAAAAGGCAAAATT 927
Db 327 CCCCTGAGTTAATGATTTGTGTGCTCTCAGATAGGGGTTTACCTCATGAACAAGATA 386
QY 928 TTAGAAATGGAAAAGTTGATTTCTGAACACGCTGACAGTTCAACATGTTCTGTTTCCAAACCT 987
Db 387 CTGGCCATGGAGAAAACCATATTAATAAGCTGGAATGGAATTTGACCTGCTGCTACACCT 446
QY 988 TATGCTTTCATCAAGAGCTTTCTGAAAGCTGCAGATGCAGATAAACAGCTTGACCTAGCG 1047
Db 447 TTTGTTTTCCTAGTTTCTGTTTATCAAGGACGGTCCAGATCAGGAGTTGGAAGAACATG 506
QY 1048 TCATTTTTCATGCTGGAGCTGCTGTTGTTGTAATACCAAAATGCTGAATTTATCGGCCCTTGG 1107
Db 507 GCTCATTTTATGCTGAGTTGGGAATGATGAACATATGCAACCTTAATGCTACTGCCCATCA 566

QY 1108 CATCTGGCTGCTGCTGGGTTTATCTGCACAGTGTGCTATCAATCGTTGCCAGACTGG 1167
Db 567 ATGTTGCTGCTCTCAGAGTGTTCAGCAAGATGCACTCTGAACAAGCTCCCTTTGG 626
QY 1168 ACAAGGCTCTGAGTCTCATAGCAGATACACTAGCAGCAAACTCTCTGGAGTGTGAGG 1227
Db 627 AATGAGACACTTAAGCTGCACACTGGTTACTCAAGAGCAACTCATGGATTGTGCTAGA 686
QY 1228 ATGATGGTAGATTTTCCACCAGAGGCTGGAACCACTAGCTCAGTGGGCTGCACAGGAG 1287
Db 687 CTATTGGTGGGTTCATTTCCACTCTTGGGAATGAAAGCTTAGGGTTGTGTACAGAAAG 746
QY 1288 TACAGTACCTACAAAGTTCCGTTGCGTGGCCAAAGATTTTGCCTGCGCAGTTCCTGTGGA 1346
Db 747 TACTCTGACCTCAGAAAGGTCAGTTGTGTGCTGCCACCTGCTAAACTTCTGCTGCTGA 805

RESULT 10

US-10-260-238-1251
; Sequence 1251, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiya
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rickes, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1251
; LENGTH: 1384
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: (610)..(610)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (668)..(668)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (676)..(676)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: N region
; LOCATION: (898)..(898)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-1251

Query Match 14.0%; Score 228.6; DB 15; Length 1384;
Best Local Similarity 56.4%; Pred. No. 1.8e-57;
Matches 482; Conservative 0; Mismatches 368; Indels 5; Gaps 3;
QY 524 AAGATCAATTTGCTCATGGATATTGACGTGCAAGCTCGGGAAACCCGTTTGTCTGCAACAG 583

Db 391 AAAAGAGCTGATATACGACATCGATGCTATCTGATGCTCACAAAGAGCTGGCAGTGATTG 450
QY 584 AATATCTTTAAAGAGCTTTTACACCTTTTACAGAGAAAATGAGCTTAAGAGTTGTGTAAGGC 643
Db 451 ATTACGTCGAAGATATCTACAGATTCTACAGAGCACTGAGAGAACACACTACCGCCCTCT 510
QY 644 CAG--ATTACATGCTCCAGGCAACAGACATATACTCAAGATGAGAGCAATTTCTGATGA 701
Db 511 CTGCACTCATGCTGTCAGACCGAGATCAACGAGAAATGAGAGCAATCTCTGACTGA 570
QY 702 CTGCTGATGAGGTTTCACTACAAAGTTTGAATCTGATGATGAGAGCTCTTTCTTATGGT 761
Db 571 TTGGCTCATCGAAGTCACTACAGGCTTATGCTGATGCCGAGAGCCCTGCTACCTCT 630
QY 762 AATCATATATGATAGATTCTTGAAAGAGAGTGGTTCAGAGAGAGCTACAATGGT 821
Db 631 CTACATAATGATCAGTACCTGCTGCTGAGAGATGTCGAGAAAGAGCTCGAGCTGT 690
QY 822 TGAGTCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
Db 691 CGAGTAAGGCCATGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 749
QY 882 GAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 941
Db 750 GGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809
QY 942 GTTGAATTCGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001
Db 810 GTCTACTTAAACAGCTCAGTGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 869
QY 1002 GAGTTTCTGAAAGCTGAGATGAGATGA--ACAGTTGAGTACGCTGCTGCTGCTGCT 1059
Db 870 TCGATACCTGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 929
QY 1060 CTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119
Db 930 GCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 989
QY 1120 GCTGCGCTTTTACTGACAGTGTGCTATCAATCGTTGCGAGCACTGGAACAAGGCTGCT 1179
Db 990 GCTGCGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1049
QY 1180 GAGTCTCATAGATACATGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1239
Db 1050 GAGTACCAACCGGCTTAGCTGAGCGCAATGCTGAGTGTGCGAGCGGCTGCTGCTGCT 1109
QY 1240 TTTTACCAGAGGCTGGAACAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1299
Db 1110 CTGCAAGCGGCGGCGGAGAGCAGGAGAGTGTGTGTAACAAGTACGCGAGCGCC 1169
QY 1300 AGTTTGGTTCGCTGCGCAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1359
Db 1170 AAGCTCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1229
QY 1360 CCGCTCTCTTCAAGT 1374
Db 1230 GTGGCGGCTTGAGCT 1244

RESULT 11

US-10-424-599-103481
; Sequence 103481, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 103481
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64461C.1
US-10-424-599-103481

Query Match 13.5%; Score 220.6; DB 12; Length 1944;

Best Local Similarity 56.9%; Pred. No. 5.8e-55;
Matches 466; Conservative 0; Mismatches 344; Indels 9; Gaps 3;

QY 529 GAATGCTCATGATATTGACAGTGGAGACTCGGGAACCCGCTTGCTGCAACAGAAATAT 588
Db 856 GAGTTTGTGATGACATTGATGCACTGACATGACAAATGAAATGGCAGCCGAGTAC 915
QY 589 GTTAAAGAGCTTTACACCTTTTACAGAGAAAATGAGCTTAAGAGTTGTGTAAGCCAGAT 648
Db 916 ATCGATGATATCTACAAATTTTACAAAGAGACTGAAGAAGATGGTTGTGT--GCATGAC 972
QY 649 TACATGTCAGCCAAACAGACATAAATCTCAAGATGAGAGCAATTTCTGATTGACTGGCTG 708
Db 973 TACATGAGTTCCGAGCCAGATATTAATGCCAAGTGAAGTCAATCTTGTGGAGTGGTGG 1032
QY 709 ATTGAGGTTCACTACAAAGTTTGAATGATGATGAGAGCGCTCTTTTATGTTAAACATA 768
Db 1033 ATAGAAGTGCATAGGAAGTTTGAGCTCATGCCAGAACTCTTTATTTGACCTTGAACATT 1092
QY 769 ATAGATAGATTCTTGGAAAAGGAGTGTTCACAGGAAGAGCTACAACTGGTTGGAGTC 828
Db 1093 GTGATCGTTTCTGCTGAGAGCTGCTGCTGAGAGGAGTGGCACACAGGTTAATGACTTT 1152
QY 829 ACAGTATGCTGCTGCTTGTAAATATGAGAGGATCTGTTCCAGTTGTGAGGACCTT 888
Db 1153 AGCTCAATGCTGATAGCTTCAAAATATGAAGAGATATGGCACACAGGTTAATGACTTT 1212
QY 889 GTGCTGATATCTGACCTGCTGCTACACAAAGGCAATTTTGAATAAGGAAAGTTCATT 948
Db 1213 GTGTGATATCAGACAAATGCTTATGTTAGTGAACAGTGTGATGATGAGGAAACAATC 1272
QY 949 CTGAACAGCTGCTGCTGCTCAACATGCTGTTCCAACTGTTATGCTTTCATGAAGAGTTT 1008
Db 1273 CTAGGAAGCTTGAATGCTTAAACAGTTTCCAACTGCTTCTTGGTTAGGTAT 1332
QY 1009 CTGAAGCTGAGAT--GCAGTAAACAGCTTGAAGTGGTGGTCAATTTTTCATGCTGAG 1065
Db 1333 ACCAAGCTTCCACTCCGCTGCAAAAGAGATGAGAAACATGGTGTGTTTCTTCTGCTGAA 1392
QY 1066 CTCTGCTTGTAGAAATACCAAA--TGCTGAATATCGGCTTCCGCTTCCGATCTGGCTGCT 1122
Db 1393 CTGGAATGATGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1452
QY 1123 GCGGTTTATCTGACAGTGTGCTATCAATGTTGCGAGCACTGGAACAAAGGCTGCGAG 1182
Db 1453 GCTGTGTTGCGGCTCGATGACCTTGGAAAGGAGCCCTTTTTCGACAAACACTTGAATG 1512
QY 1183 TCTCATAGCATACACTAGCGACCACTCTCTGAGTGTCTCGAGATGATGATGATGATTT 1242
Db 1513 CACTACACAGGCTACTCTGAGGCAACTAAGGATTTGGGCCAAATCATGGCCAACTT 1572
QY 1243 CACCAAGAGGCTGGAACACAGTAAAGTCTACTGCTGCTGACAGGAGTACAGTACCTACAG 1302
Db 1573 CATGCTGCTGCAACAGGAAAGTAAAGCTTAGGCGAGTTTACAGAAATTTCTTAACTCGAT 1632
QY 1303 TTCGTTTGGTGGCCAGAAATTTTGTGCTGCGAGTTTCTCTG 1341
Db 1633 CTTTCTGCTGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1671

RESULT 12

US-10-424-599-118855
; Sequence 118855, Application US/10424599

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Db      1368  TTTCTACTCCACTCTTGAGAAATGGAAGCTTAGGGTTGTGTCGGAATAATTCTGACCT 1427
QY      1300  AAGTTCGGTGTGGTGGCCAGATTTTGGCTGCGCAGTTCTCTGCTG 1344
Db      1428  CAGAAGGGTGCTGTTGCTGTGTCTCCACCCGCTAAATTTCTTCTG 1472

RESULT 13
US-09-938-842A-789
; Sequence 789, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 789
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-789

```

Query Match	13.1%;	Score 214.6;	DB 9;	Length 1338;
Best Local Similarity	54.5%;	Pred. No. 2.8e-53;		
Matches 452;	Conservative 0;	Mismatches 374;	Indels 3;	Gaps 1;
QY	516	TATGAACGAAGATGAATTCCTCATGTGATATTCAGACGTGCAGACTCGCGGGAACCGGTTCG	575	
DB	474	TATAGTCAACAACCAAGATTCATCGATTTGATGAATCTGACAAAGATAACCATTTGGC	533	
QY	576	TGCAACAGAAATATGTTAAAGAGCTTTACACCTTTTACAGAGAAAATAGAGCTAAGAGTTG	635	
DB	534	TGCGGTGGAGTATGTTGATGATATGTACTCGTTCTTATAAAGAGTTTGAGAAGGAGAGTCA	593	
QY	636	TGTAAGGCCAGATTACATCTCCAGCCAAACAAGACATAAACTCAAAGATGAGAGCAATTC	695	
DB	594	GCTTAGATG---TACATGCACATTCGACTGAAATGATGAGAAGATGAGACGATCTT	650	
QY	696	GATTGACTGGCTGATTGAGGTTTCACCAAGTTTGAACTGATGGATGAGACGCTCTTTCT	755	
DB	651	GATTGATTGGTTACTAGAAGTTACATCAAGTTTGAGCTCAACCTTGAACCTCTGTACCT	710	
QY	756	TATGTTAAACATAATAGATAGATTCTTGGAAAGGAAGTGGTTCCAAGGAGAGCTACA	815	
DB	711	CACCGTCAACATCATTTGATCGATTCCTCTCTGTGAAAGCTGTCCCTTAAGAGAGATTACA	770	
QY	816	ACTGGTTGGAGTCCACAGCTATGCTGCTCGCTTGTAATATGAGGAGGTATCTGTTCCAGT	875	
DB	771	GCTAGTGGGAATCAGTGCCTTGCTTATTCGTTCCAAATATGAAGAAATCTGGCCACCTCA	830	
QY	876	TGTTGAGGACCTTGCTGATATCTCACCGTGCCTACACAAGGGCAATTTTAGAAT	935	
DB	831	GGTTAACGATCTGGTGATATGTCAACGGACAATGCTTACAGTAGCAGACAGATTCGTGTGAT	890	
QY	936	GGAAAAAGTTGATTCTGAAACAACGCTGCAGTTCACATGTCGTGTTCCCAACACTTATGTCTT	995	
DB	891	GGGAAGGCAATTCCTTGGAAACCTCGAATGGTATTTGACAGTCCCGACTCAATACGTCCT	950	
QY	996	CATGAAGAGGTTCTTGAAAGCTGCAGATGCAGATAAACAGCTTGAGCTACGGTCATTTTT	1055	

APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchikanti
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidy, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 52
LENGTH: 1850
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (254)..(1579)
OTHER INFORMATION:
US-10-310-154-52

Search completed: March 20, 2004, 23:16:41
Job time : 590 secs

Query Match 13.0%; Score 212.8; DB 15; Length 1850;
Best Local Similarity 56.6%; Pred. No. 1.2e-52;
Matches 466; Conservative 0; Mismatches 337; Indels 21; Gaps 3;
Qy . 530 AATTGCTCAGGATGATGACAGTGCAGACTCGGGGAAACCGCTTGTGTCACACAGATATG 589
Db 747 AAGTGGTCGATGACATCGACAAAGCTGGACGCTCAACATGAGCTCGCGGTGGTGAATACA 806
Qy . 590 TTAAGAGCTTTACACCTTTTACAGAGAAATGAGGCTAAGAGTTGTGTAAGGCCAGATT 649
Db 807 TTGAGGACATCTACAGTTCTACAGATTGCTCAGACGAGAGACGCCATG---TGACT 863
Qy . 650 ACATGTCCAGCAACAAGACATAAACTCAAAGATGAGAGCAATCTGAATTGACTGGCTGA 709
Db 864 ACATCGACGCCAACTCGAGATCAACTCTAAGATGAGGCTATCTTGGCTGATTGGATAA 923
Qy 710 TTGAGGTTCACTACAAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 769
Db 924 TTGAAGTACACCAAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 983
Qy 770 TAGATAGATTCTTGGAAAAGAGTGGTTCCAGAGAAAGAGTGAAGTGAAGTGAAGTGAAGTGA 829
Db 984 TCGATCAGTACCTCTCGCTGCAACAGTCTCGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGA 1043
Qy 830 CAGCTATGCTGCTCGCTGTAATATGAGAGGATATCTGTTCCAGTTGTTGAGGACCTTG 889
Db 1044 CATCTATGCTGATCGCTGCAAGTACGAGGAGATTTCGGCCCCCAGAGGTGAACGACTTCA 1103
Qy 890 TGCTGATATCTGACCGCTCTACACAAAAGGGCAAAATTTAGAAATGAAAAGTTGATTC 949
Db 1104 TCCTCATATCAGACAGTGCATACAGTAGAGAACAGATTCTTCGATGAGAGAGGGAATTC 1163
Qy 950 TGAACAGCTCAGTTCAACATGCTGTTCCAAACCTTATGCTTTCATGAAGAGGTTTC 1009
Db 1164 TGAATAGGCTGGAGTGAACCTGACTGTCCTACAGTGTATATGTTCTTTCCTGCTGCTTTC 1223
Qy 1010 TGAAGCTGTCAG-----ATGAGATAAACAGCTTGAGCTAGCTGCTCAATTTTCA 1057
Db 1224 TGAAGGCCGCAACATTGGCCGCGCAAGTTGAGAAAGAGATGAGAAATATGCTGCTTCT 1283
Qy 1058 TGCTGGAGCTCTGCTTGGTAGAATACCAATGCTGAATATTTCGGCCCTTCGCACTCTGGCTG 1117

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 20, 2004, 19:33:10 ; Search time 4447 Seconds
(without alignments)
10985.952 Million cell updates/sec

Title: US-09-496-444-1
Perfect score: 1636
Sequence: 1 tcacggggctctccgtccg.....aaaaaaaaaaaaaaaaaaaaa 1636

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_htc.*
- 9: gb_estl.*
- 10: gb_est2.*
- 11: gb_htc.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estcom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_nam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vrl.*
- 28: gb_gsl.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1534	99.9	1655	11	AY104859
2	598.8	36.6	863	14	CA280467
3	597.2	36.5	613	14	CD001829
4	596	36.4	607	10	AW256237

C	5	585.8	35.8	589	12	BG268357
	6	579	35.4	579	14	CD001830
	7	570.2	34.9	574	14	CA249171
	8	552	33.7	563	13	CA122466
	9	531.6	32.5	586	9	AI770352
C	10	512.6	31.3	742	13	CA122563
C	11	502.4	30.7	683	14	CA223571
C	12	485.2	29.7	778	29	CG453107
C	13	485.2	29.7	779	29	CG453099
C	14	485.2	29.7	873	29	CG278953
	15	482	29.5	626	13	CA101841
	16	471.4	28.8	625	13	CA085373
	17	469.2	28.7	646	14	CA223491
	18	463	28.3	463	10	B638542
C	19	462.8	28.3	553	14	CF036794
C	20	452	27.6	717	14	CA299622
	21	450	27.5	631	13	CA083532
C	22	443.4	27.1	690	14	CF625999
	23	430.4	26.3	577	14	CA292585
	24	429.6	26.3	623	14	CB882198
C	26	423.4	25.9	956	29	CG214272
C	27	420.2	25.7	868	29	CG293488
	28	418.4	25.6	982	10	B8040145
	29	411.2	25.1	580	14	CA269779
	30	410	25.1	944	29	CG293502
	31	402	24.6	525	12	B1099542
	32	390	23.8	608	14	CA831492
C	33	387.6	23.7	564	14	CA292710
	34	386.4	23.6	817	14	CB000327
	35	384.4	23.5	1643	11	AV111119
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	37	357.4	21.8	490	12	B1411133
	38	339.8	20.8	686	14	CA253051
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C	40	326.2	19.9	400	13	BQ538226
C	41	326.2	19.9	507	13	BUI101379
	42	320	19.6	615	14	CA242395
	43	314.6	19.2	666	13	CA074749
	44	309	18.9	596	14	CA999572
	45	307.6	18.8			

ALIGNMENTS

RESULT 1	AY104859	AY104859	1655 bp	mRNA	linear	HTC 16-OCT-2002
LOCUS	Zea mays PC0144752 mRNA sequence.					
DEFINITION	Zea mays PC0144752 mRNA sequence.					
ACCESSION	AY104859					
VERSION	AY104859.1 GI:21207937					
KEYWORDS	HTC.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
REFERENCE	1 (bases 1 to 1655)					
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 1655)					
AUTHORS	Coe, E.H.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the					

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CD001830	3529 1.10
CA249171	SCSBL110
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CA223491	SCJFFL1C0
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CA269779	SCMCR308
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ORIGIN

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Qy	421	G	C	G	A	T	G	C	A	C	C	G	T	T	G	A	T	T	C	A	C	C	T	G	A	A	C	T	C	T	C	A	C	A	G	C	T	G	T	C	A	G	C	T	480	
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Qy	481	G	A	C	A	T	C	A	T	G	G	T	C	G	A	C	A	G	A	A	C	A	A	G	A	C	A	T	T	A	G	A	C	A	A	G	A	T	G	A	A	T	G	C	T	540
Db	500	G</																																												

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.

1 (bases 1 to 863)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: C09 row: F column: 11

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..863

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCVPFL1C09F11"

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/clone_lib="FL1"

/note="Organ: Inflorescence at beginning of development

(1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;

An unidirectional cDNA library generated from

inflorescence at beginning of development (1cm-long)].

cDNA was prepared from polyA+ mRNA using SuperScript

plasmid system kit (Invitrogen). The double-strand cDNAs

were fractionated in a sepharose CL-2B 40cm-columns and

fragments sizing between 0.8 and 1.5 Kb were

directionally cloned into the vector. Details of each

source of RNA and library construction can be obtained at

http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 36.6%; Score 598.8; DB 14; Length 863;
Best Local Similarity 92.2%; Pred. No. 2.9e-80;
Matches 642; Conservative 0; Mismatches 52; Indels 2; Gaps 1;

QY 881 AGGACCTTGTGCTGATATCTACCGTGCCTACACAAAGGCCAAATTTAGAAATGAAA 940
DB 1 AGGACCTTGTGCTATTTCTGATCTGCTGCCTACACAAAGGCCAAATTTAGAAATGAAA 60

QY 941 AGTTGATTCGAACAGCTGCAGTCAACATGTCTGTTCCACACCTTATGCTTCATGA 1000
DB 61 AGTTGATTCGAACAGCTGCAGTCAACATGTCTGTTCCACACCTTATGCTTCATGA 120

QY 1001 AGAGGTTTCTGAAGCTGCAGATGCAGATAAACAGCTTGAGCTAGCGTCAATTTTCATGC 1060
DB 121 AGAGGTTTCTGAAGCTGCAGATGCAGATAAACAGCTTGAGCTAGCTAGCTTCATGC 180

QY 1061 TGGAGCTCTGCTTGTAGATACCAAGCTGTAATTCGGCTTCGGATCTGGCTGCTG 1120
DB 181 TGGAGCTCTGCTTGTAGATACCAAGCTGTAATTCGGCTTCGGATCTGGCTGCTG 240

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DB 241 CTGCGGTTTATCTCCAGTGTGCTATCAATCGTTGCCAGCACTGGACAAAGGCTCTGCG 300

QY 1181 AGTCTCATAGCAGATACACTAGCGACCAACTCTCGAGTGTCTGAGGATGATGTAGATT 1240
DB 301 AGTCTCATAGCAGATACACTAGCGACCAACTCTCGAGTGTCTGAGGATGATGTAGACT 360

QY 1241 TTCACAGAGGCTGGAAACAGTAAAGCTCACTGGGGTGCACAGGAAGTACAGTACCTACA 1300
DB 361 TTCACAGAGGCTGGAAACAGTAAAGCTCACTGGGGTGCACAGGAAGTACAGTACCTACA 420

QY 1301 AGTTCCGTTGCTGGCCCAAGATTTTTCCTGCGCGCATTTCTCTGCTGGAGTCTGGAGGACAC 1360

DB 421 AGTTCCGTTGCTGGCCCAAGACTTTTCGCGCGCATTTCTGCTGGAGTCTGGAGGACAC 480
QY 1361 CGCCTCTCTTCAGGTGCAAACTAGTTGAATTCGACCTATTCAACTGGGTG--GATTTTTTAA 1418
DB 481 CGCCTCTCTTCAGGTGCAATCTAGTTGAATTCGACCTATTCAACTGGGTGATTTTTTA 540
QY 1419 AGTTTGTAGAACTCTCCATGAACAAGATGCAGAAAACATCGTTGTGATGTTGCCCAAG 1478
DB 541 AGTTTGTAGCACTACTCCGTGGAACAAGATGCAGAAAACATCGTTGTGATGTTGCCCAAG 600
QY 1479 TGCATCGAAATTTCTTTGGAGAGTATGATTAACAATTTTATTTTATCTATCTTGAATGA 1538
DB 601 TGCATCGAAATTTCTTTGGAGAGTATGATTAACAATTTTATTTTATCTATCTTGAATGA 660
QY 1539 CGAGTACCGTCTCGTGCACGTTGTGCTTGTGCAATTA 1574
DB 661 CGAGTACCGTCTCGTGCAGGTCGTTTACTGCGGCTA 696

RESULT 3

CD001829/c

LOCUS

DEFINITION

3529_1.104_1.D01.X.1 3529 - 2 mm ear tissue from Schmidt and Hake

labs Zea mays cDNA, mRNA sequence.

CD001829

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 613)

AUTHORS

Walbot V

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 3529.1.104.1 row: D column: 01.

Location/Qualifiers

1..613

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/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake

labs"

/note="Organ: ear; Vector: PAD-CAL4-2.1; Site 1: EcoRI;

Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu

amplified. Ampicillin is the selection marker."

ORIGIN

Query Match 36.5%; Score 597.2; DB 14; Length 613;

Best Local Similarity 99.3%; Pred. No. 6e-80;

Matches 610; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 825 AGTCACAGTATGCTCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGA 884

DB 613 AGTCACAGTATGCTCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGA 554

QY 885 CTTTGTGCTGATATCTGACCGTGCCTACACAAAGGGCAATTTTAGAAATCGAAAAGTT 944

DB 553 CTTTGTGCTGATATCTGCGCTGCCCTACACAAAGGGCAATTTTAGAAATCGAAAAGTT 494

QY	945	GATTCTGAA	CAGCGTCGAGTTCAACATGCTGTTCCACACCTTATGCTTTCATGAAGAG	1004
Db	493	GATTCTGAA	CAGCGTCGAGTTCAACATGCTGTTCCAAACCCCTATGCTTTCATGAAGAG	434
QY	1005	GTTCCTGAA	AGCTGCAGATGCAGATAAACAGAGTTCGAGCTAGCGTCAATTTTTCATGCTGGA	1064
Db	433	GTTCCTGAA	AGCTGCAGATGCAGATAAACAGAGTTGAGCTAGCGTCAATTTTTCATGCTGGA	374
QY	1065	GCTCTGCTT	GTTGTAATACCAATGCTGAATTTATCGGCTTCGCATCTGGCTGCTGCTGC	1124
Db	373	GCTCTGCTT	GTTGTAATACCAATGCTGAATTTATCGGCTTCGCATCTGGCTGCTGCTGC	314
QY	1125	GGTTTATA	CTGCACAGTGTCTATCAATCGTTGCCAGCACTGGACAAAGTCTCGAGTC	1184
Db	313	GGTTTATA	CTGCACAGTGTCTATCAATCGTTGCCAGCACTGGACAAAGTCTCGAGTC	254
QY	1185	TCATAGCAG	ATACACTAGCGACCAATCTCTGGAGTGTCTCGAGGATGATGGTAGATTTTCA	1244
Db	253	TCATAGCAG	ATACACTAGCGACCAATCTCTGGAGTGTCTCGAGGATGATGGTAGATTTTCA	194
QY	1245	CCAGAGGCT	GGAACCAAGTAAAGTCTACTGGCTGCACAGGAAGTACCTACAAGTT	1304
Db	193	CCAGAGGCT	GGAACCAAGTAAAGTCTACTGGCTGCACAGGAAGTACCTACAAGTT	134
QY	1305	CGGTTGGTG	GCCAAGATTTTTCCTGCGCAGTTCCTGCTGGAGTCGGAGGAGCACCGCC	1364
Db	133	CGGTTGGTG	GCCAAGATTTTTCCTGCGCAGTTCCTGCTGGAGTCGGAGGAGCACCGCC	75
QY	1365	TCCTTCAGG	TGCACCTAGTTGAATGCACCTATTCAACTGGGTGGATTTTAAAGTTT	1424
Db	74	TCCTTCAGG	TGCACCTAGTTGAATGCACCTATTCAACTGGGTGGATTTTAAAGTTT	15
QY	1425	TAGAATACT	CCATG 1438	
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[illegible]

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FEATURES
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Plate: 687075 row: H Column: 12.
Location/Qualifiers
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/organism="Zea mays"
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/db_xref="taxon:4577"
/tissue_type="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli: 50Lg"

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/clone lib="687 - Early embryo from Delaware"
/note="Organ: embryo; Vector: pBluescript SK; Site: 1:
XhoI; Site 2: EcoRI; Library was prepared by Statagene
using the Uni-ZAP XR system (Stratagene BN93728-12).
Clones were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"

ORIGIN

Query Match	36.4%;	Score 596;	DB 10;	Length 607;
Best Local Similarity	100.0%;	Pred. No. 9e-80;		
Matches 596;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	969	CATGTCGTGTTCCAAACACCTTATGCTCTTCATGAAGAGGTTTCTGAAGAGCTGCAGATGCAGA	1028	
Db	607	CATGTCGTGTTCCAAACACCTTATGCTCTTCATGAAGAGGTTTCTGAAGAGCTGCAGATGCAGA	548	
QY	1029	TAAACAGCTTGAGCTAGCTAGCTATTTTTCATGCTGGAGCTCTGCTTGGTAGAATACCAAT	1088	
Db	547	TAAACAGCTTGAGCTAGCTAGCTATTTTTCATGCTGGAGCTCTGCTTGGTAGAATACCAAT	488	
QY	1089	GCTGAATATPCCGCCCTTCGCATCTGGCTGCTGCTGCGGTTTATACCTGCACAGTGTGCTAT	1148	
Db	487	GCTGAATATPCCGCCCTTCGCATCTGGCTGCTGCTGCGGTTTATACCTGCACAGTGTGCTAT	428	
QY	1149	CAATCGTGTCCAGCACTCGACAAAGAGCTCGGAGTCTCATAGCAGATACACTAGCGACCA	1208	
Db	427	CAATCGTGTCCAGCACTCGACAAAGAGCTCGGAGTCTCATAGCAGATACACTAGCGACCA	368	
QY	1209	ACTCGGAGTGCTCGAGGATGATGGTAGATTTTTCACAGAGGCTGGAAACCAAGTAAAGCT	1268	
Db	367	ACTCGGAGTGCTCGAGGATGATGGTAGATTTTTCACAGAGGCTGGAAACCAAGTAAAGCT	308	
QY	1269	CACGTGGGTGCACAGGAAGTACAGTACCTACAAGTTCGGTTGCGTGCCCAAGATTTTGGC	1328	
Db	307	CACGTGGGTGCACAGGAAGTACAGTACCTACAAGTTCGGTTGCGTGCCCAAGATTTTGGC	248	
QY	1329	TGGCAGATTTCCTGCTGGAGTCGGGAGGAGACACCGCTCTCTTCAGGTGCGAAACTAGTTGAA	1388	
Db	247	TGGCAGATTTCCTGCTGGAGTCGGGAGGAGACACCGCTCTCTTCAGGTGCGAAACTAGTTGAA	188	
QY	1389	TCGACCTATTCAACTCGGTGGATTTTTTAAAGTTTTTAAAGTACTCCATGAACAAGATGC	1448	
Db	187	TCGACCTATTCAACTCGGTGGATTTTTTAAAGTTTTTAAAGTACTCCATGAACAAGATGC	128	
QY	1449	AGAAACATCGTGTGATGTTGCCCAAAGTGATCGAATTTCTTTTGGAGAGTTATGATT	1508	
Db	127	AGAAACATCGTGTGATGTTGCCCAAAGTGATCGAATTTCTTTTGGAGAGTTATGATT	68	
QY	1509	AACAACTTTTTTTTTTATCTATGTTGAATGACAGGTGACGGTCGGTCAAGTTGTGCT	1564	
Db	67	AACAACTTTTTTTTTTATCTATGTTGAATGACAGGTGACGGTCGGTCAAGTTGTGCT	12	

RESULT 5	ACCESSION	REFERENCE
BG268357/c	VERSION	
LOCUS	KEYWORDS	
DEFINITION	SOURCE	
	ORGANISM	

AUTHORS Walbot V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL University
 COMMENT Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1000174 row: E column: 12.
 Location/Qualifiers
 1..589
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:4577"
 /clone_lib="1000 - Unigene I from Maize Genome Project"
 /note="This library represents the unique ESTs found in the first round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 486, 487, 496, 603, 605, 614, 618, 660, 683, 687, 707, and 945. Contigs were assembled using TIGR's CAP program and a representative EST from each contig was selected for the Unigene set. All singlets were also selected."
 ORIGIN
 Query Match 35.8%; Score 585.8; DB 12; Length 589;
 Best Local Similarity 99.7%; Pred. No. 3.1e-78;
 Matches 587; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 942 GTTGATTTCTGAACAGCTGCATTCACATGCTCTTTCACACACCTTATGCTTCATGAA 1001
 Db 589 GTTGATTTCTGAACAGCTGCATTCACATGCTCTTTCACACACCTTATGCTTCATGAA 530
 QY 1002 GAGTTTCTGAAAGCTGCAGATGAGATAAAGCTTGTAGCTAGCTGATTTTTCATGCT 1061
 Db 529 GAGTTTCTGAAAGCTGCAGATGAGATAAAGCTTGTAGCTAGCTGATTTTTCATGCT 470
 QY 1062 GGAGCTCTCTTGGTAGAATACCAATGCTGAATTTATCGGCTTCGCATCTGGCTGTCG 1121
 Db 469 CGAGCTCTCTTGGTAGAATACCAATGCTGAATTTATCGGCTTCGCATCTGGCTGTCG 410
 QY 1122 TCGGTTTATCTGCACAGTGTCTTCAATGCTTGGCAGACTGCAGAAAGCTGCGA 1181
 Db 409 TCGGTTTATCTGCACAGTGTCTTCAATGCTTGGCAGACTGCAGAAAGCTGCGA 350
 QY 1182 GTCTCATAGCAGATACACTAGCGACCAACTCTCGAGTGTCTCGAGGATGATGTAGATT 1241
 Db 349 GTCTCATAGCAGATACACTAGCGACCAACTCTCGAGTGTCTCGAGGATGATGTAGATT 290
 QY 1242 TCACGAGAGGCTGGNACAGTAAGCTCACTGGCTGCACAGAAAGTACGTACCTACAA 1301
 Db 289 TCACGAGAGGCTGGNACAGTAAGCTCACTGGCTGCACAGAAAGTACGTACCTACAA 230
 QY 1302 GTTCGGTTGCTGGCCCAAGATTGCTCGCAGATTCTGCTGGAGTGGGAGGACACC 1361
 Db 229 GTTCGGTTGCTGGCCCAAGATTGCTCGCAGATTCTGCTGGAGTGGGAGGACACC 170
 QY 1362 GCCTCCTTCAGGTGCAAACTAGTTGAATCGACTATTCGAATCGGTGGATTTTTAAAGT 1421
 Db 169 GCCTCCTTCAGGTGCAAACTAGTTGAATCGACTATTCGAATCGGTGGATTTTTAAAGT 110
 QY 1422 TTTTGAATCTCCTGAACAGATCGCAAAACATCGTTGATGTTGTCGCCAAAGTGC 1481
 Db 109 TTTTGAATCTCCTGAACAGATCGCAAAACATCGTTGATGTTGTCGCCAAAGTGC 50
 QY 1482 ATCGAATTTCTTGGAGAGTTATGATTAACAATTTTTTTTTTATCTATG 1530
 Db 49 ATCGAATTTCTTGGAGAGTTATGATTAACAATTTTTTTTTTATCTATG 1

RESULT 6
 LOCUS CD001830
 DEFINITION 3529_1_104_1.D01.y.1 3529 - 2 mm ear tissue from Schmidt and Hake
 labs Zea mays cDNA, mRNA sequence.
 ACCESSION CD001830
 VERSION
 KEYWORDS EST.
 SOURCE CD001830.1 GI:30307157
 ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 579)
 AUTHORS Walbot V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL University
 COMMENT Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3529_1_104_1 row: D column: 01.
 Location/Qualifiers
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 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="ear"
 /dev_stage="2 mm"
 /lab_host="E. coli XL0LR"
 /clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
 labs"
 /notes="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI;
 Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
 amplified. Ampicillin is the selection marker."
 ORIGIN
 Query Match 35.4%; Score 579; DB 14; Length 579;
 Best Local Similarity 100.0%; Pred. No. 3.2e-77;
 Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 TCCTCCGTCGTTAAGCACCGCGCAGCGTCTCGGTGGATCAACAGCGCGCGATCCG 69
 Db 1 TCCTCCGTCGTTAAGCACCGCGCAGCGTCTCGGTGGATCAACAGCGCGCGATCCG 60
 QY 70 TCTTCTTCCCTCTCTCTCGGGTTCGGGATCATGGCGCGCGGGCGGTGAC 129
 Db 61 TCTTCTTCCCTCTCTCTCGGGTTCGGGATCATGGCGCGCGGGCGGTGAC 120
 QY 130 GAGAACAGGAGACCGCGGAGAGCCCGCCAGGCGTCCGACACATGGCGAGCGG 189
 Db 121 GAGAACAGGAGACCGCGGAGAGCCCGCCAGGCGTCCGACACATGGCGAGCGG 180
 QY 190 CGGCGCTCACGACATCAAGAACCTCGTCGGGGTCCCGCTACCCCTACGCGGTGCC 249
 Db 181 CGGCGCTCACGACATCAAGAACCTCGTCGGGGTCCCGCTACCCCTACGCGGTGCC 240
 QY 250 AAGAACGCCATGTGCAAGAGACAAAGGAGCGAAAGCAGCCAGCGTTGGCAAGCAGC 309
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 QY 310 CGGCCATGACAGGAATTCGCGCTCTTCGCGAGCAAGGCGCAACTGTAATGTGAG 369
 Db 301 CGGCCATGACAGGAATTCGCGCTCTTCGCGAGCAAGGCGCAACTGTAATGTGAG 360
 QY 370 CCGATCGTAGTCATCCAGAACCCGAAGTTGTCAACAGAGGAATCAGTAGCGGTGCG 429

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Db 361 CCGATGCTAGTCTGATCCAGAACCCGGAAGTTGTCAACAGAGGAATCAGTAGGCGATGC 420
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Db 421 ACCGTTGATATTGACGTGGAACTCTACGAGCTGGTTCGACGGTAGTGATAGTACATCGAC 480
Qy 490 ATGGGTGCGACAGACAGAACAGGACATTATGAACGAAGATGAATTGCTCATGATATTGAC 549
Db 481 ATGGGTGCGACAGACAGAACAGGACATTATGAACGAAGATGAATTGCTCATGATATTGAC 540
Qy 550 AGTGCAGACTCGGGGACCCGCTTGTCTGCAACAGAAATAT 588
Db 541 AGTGCAGACTCGGGGACCCGCTTGTCTGCAACAGAAATAT 579

RESULT 7
CA249171
LOCUS SCSEBFL1107F08.9 FL1 Saccharum officinarum cDNA clone SCSBFL1107F08
DEFINITION 5', mRNA sequence.
ACCESSION CA249171
VERSION CA249171.1 GI:353331564
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 674)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 107 row: F column: 08
Seq primer: T7 Promoter Primer.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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/clone="SCSEBFL1107F08"
/lab_host="DH10B"
/clone_lib="FL1"
/notes="Organ: Inflorescence at beginning of development
(lcm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
An unidirectional cDNA library generated from
[Inflorescence at beginning of development (lcm-long)].
cDNA was prepared from polyA+ mRNA using Superscript
Plasmid System kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

Query Match 34.9%; Score 570.2; DB 14; Length 674;
Best Local Similarity 31.1%; Pred. No. 6.3e-76;
Matches 614; Conservative 0; Mismatches 58; Indels 2; Gaps 1;

Qy 881 AGGACCTTGCTGATATCTGACCGTCCATACAAAGGGCAAAATTTAGAAATGAAA 940
Db 1 AGGACCTTGCTGATTTCTGATCGTCTACACAAAGGGCAAAATTTAGAAATGAAA 60

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Qy 941 AGTTGATTTCTGACACGCTGCAGTTCAACATGTTGTTCACACACCTTATGTCTTCATGA 1000
Db 61 AGTTGATTTCTGACACGCTGCAGTTCAACATGTTGTTCACACACCTTATGTCTTCATGA 120
Qy 1001 AGAGGTTTCTGAAAGCTGCAGATGACAGATAAAGCAGCTGTAGCTAGCTCAATTTTCAAGC 1060
Db 121 AGAGGTTTCTGAAAGCTGCAGATGACAGATAAAGCAGCTGTAGCTAGCTCAATTTTCAAGC 180
Qy 1061 TGGAGCTCTGCTGGTGGTAAATACCAATGCTGAATATATCGCCCTTCGCATCTGCTGCTG 1120
Db 181 TGGAGCTCTGCTGGTGGTAAATATCAAAATGCTGAATATCAAGCTTCGCATCTGCTGCTG 240
Qy 1121 CTGCGGTTTATACATGACAGTGTGCTATCAATCGTTGCCAGCAGCTGACAAAAGTCTGCG 1180
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Qy 1181 AGTCTCATAGCAGATACACTAGCGCAACACTCTGCGAGTCTCGAGGATGATGCTAGATT 1240
Db 301 AGTCAATAGCAGATACACTAGCGCAACACTCTGCGAGTCTCGAGGATGATGCTAGATT 360
Qy 1241 TTCAACAGAGCTTGGAAACCAAGTAAGCTCACTGCGTGCACAGGAAGTACAGTACCTTACA 1300
Db 361 TTCAACAGAGCTTGGAACTGGCAAGCTCACTGCGTGCACAGGAAGTACAGTACCTTACA 420
Qy 1301 AGTTGCGTGTGCTGCGCAAGATTTTCTGCGAGTCTCTGCGAGTCTCTGCGAGTGGAGGAC 1360
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Qy 1361 CGCTCTCTTCAAGTGCACAACTAGTTGAATGCACTTATCACTTCACTTCACTTCACTTCA 1418
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Qy 1419 AGTTTGTAGATATCTCCATGACCAAGATGCAAGATGCAAGAAACATGTTGATGTGCTCC 1478
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Qy 1479 TGCAATCGAATTTCTTGGAGAGTTATGATTAAACAATTTTTTTTATCTATGTTGAATGA 1538
Db 601 TGCAATCGAATTTCTTGGAGAGTTATGATTAAACAATTTTTTTTATCTATGTTGAATGA 660
Qy 1539 CGAGTGCAGGTCGG 1552
Db 661 CGAGTGCAGGTCGG 674

RESULT 8
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LOCUS SCULLR1033H06.g LR1 Saccharum officinarum cDNA clone SCULLR1033H06
DEFINITION 5', mRNA sequence.
ACCESSION CA122466
VERSION CA122466.1 GI:34975774
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 663)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 033 row: H column: 06

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Db 361 ACAAAGGCAATTCAGAAATGGAAGATTTGATCTGAACACGCTGCAATTCACATG 420
 QY 973 TCTGTTCCACACCTTATGCTTCATGAAGAGGTTTCTGAAGCTGCAGATCCAGATAAA 1032
 Db 421 TCTGTTCCACACCTTATGCTTCATGAAGAGGTTTCTGAAGCTGCAGATCCAGATAAA 480
 QY 1033 CAGCTTGAGCTAGCGTCATTTTCATGCTGGAGCTCTGCTTGGTGAATACCAATGCTG 1092
 Db 481 CAGCTTGAGCTAGCGTCATTTTCATGCTGGAGCTCTGCTTGGTGAATACCAATGCTG 540
 QY 1093 AATTATCGGCTCGGATCGGCTGCTGCTGGGTTTATCTACTGCAC 1138
 Db 541 AATTATAGGCTTCACATCGGCTGCGCTGCGGTTTATCTACTGCAC 586

RESULT 10
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 LOCUS SCJFFL1C03H06.b LRI Saccharum officinarum cDNA clone SCJLLR1033H06
 DEFINITION 3', mRNA sequence.

ACCESSION CAL122563
 VERSION CAL122563.1 GI:34975871
 KEYWORDS EST.

SOURCE

ORGANISM

Saccharum officinarum
 Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Saccharum.

1 (bases 1 to 742)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 033 row: H column: 06

Seq primer: SP6 Promoter primer.

Location/Qualifiers

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/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCJLLR1033H06"

/lab_host="DH10B"

/clone_lib="LR1"

/notes="Organ: Leaf roll from field grown adult plants

(large insert library); Vector: pSPORT1; site: 1; SalI;

Site 2: NotI; An unidirectional cDNA library generated

from [leaf roll from field grown adult plants (large

insert library)]. cDNA was prepared from polyA+ mRNA

using SuperScript Plasmid System Kit (Invitrogen). The

double-strand cDNAs were fractionated in a sepharose

CL-2B 40cm-columns and fragments sizing between 0.8 and

1.5 Kb were directionally cloned into the vector. Details

of each source of RNA and library construction can be

obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 31.3%; Score 512.6; DB 13; Length 742;

Best Local Similarity 89.4%; Pred. No. 2.5e-67;

Matches 613; Conservative 0; Mismatches 55; Indels 18; Gaps 5;

QY 925 ATTTAGAAATGGAAGTTGATCTGAACACGCTGCAGTTCAACATGCTGTCCACAA 984

Db 742 ATCTAAGAAATGGAAGTTGATCTGAACACGCTGCAGTTCAACATGCTGTCCACAA 683

QY 985 CCTATGTCTTCATGAAGAGTTTCTGAAAGCTGCAGATGACATAAACAGCTTGAGCTA 1044
 Db 682 CCTATGTCTTCATGAAGAGTTTCTGAAAGCTGCAGATGACATAAACAGCTTGAGCTA 623
 QY 1045 GCGTCA-TTTTTCATGCTGAGCTCTGCTTGGTAGAATA-CCAAATGCTGAAATATCGG 1102
 Db 622 GTGTCATTTTTCATGCTGAGCTCTGCTTGGTAGAATA-CCAAATGCTGAAATATCAGC 563
 QY 1103 C-TTCGATCTGGCTGCTGCTGGGTTTATATGACAGTGTCTATCAATCTGTCGAG 1161
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 Db 502 CACTGGACAAAGCTTTCGAGTCTCATAGCAGATACACTAGCGCAACCTCCCTGGAGTGC 443
 QY 1222 TCGAGGATGATGTTAGATTTTTCACCAAGAGCTGGAAACCAAGTCACTGCGGTGCAC 1281
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 QY 1458 CGTGTTCATGTTGCCCAAAAGTGCATCGAATTTCTTTGGAGAGTTATGATTAACAACATTT 1517
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 QY 1518 TTTTTCATGTTGAATGACGAGTACCGTTCGCTACGTTGCTGTTGTCAGTTATAC 1577
 Db 142 TTTTTCATGTTGAATGACGAGTACCGTTCGCTACGTTGCTGTTGTCAGTTATAC 94
 QY 1578 TCGCGCTAATAACAACTGTCAGTT 1603
 Db 93 TCGCGCTAATAACGACTGTCCTGTT 68

RESULT 11

CAL223571/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA223571

SCJFFL1C03E09

3', mRNA sequence.

CA223571.1

GI:35280031

EST.

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae;

Streptophyta; Embryophyta;

Tracheophyta; Tracheophyta;

Spermatophyta; Magnoliophyta;

Liliopsida; Poales; Poaceae;

PACCAD

clade; Panicoideae; Andropogoneae;

Saccharum.

1 (bases 1 to 683)

Vettore,A.L., da Silva,F.R.,

Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

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Plate: C03 row: E column: 09
Seq primer: SP6 Promoter primer.
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/lab_host="DH10B"
/clone_lib="Fli"
/notes="Organ: Inflorescence at beginning of development
(icm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI;
An unidirectional cDNA library generated from
inflorescence at beginning of development (icm-long).
cDNA was prepared from polyA+ mRNA using Superscript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details
source of RNA and library construction can be obtained at
http://sucet.lad.ic.unicamp.br/public"

ORIGIN
Query Match 30.7%; Score 502.4; DB 14; Length 683;
Best Local Similarity 91.2%; Pred. No. 8.9e-66; Indels 13; Gaps 2;
Matches 560; Conservative 0; Mismatches 41;

QY 992 TCTTCATGAAGAGGTTCTGAAAGCTGCAGATGCAGATAAACAGCTTGAGCTAGCGTCAT 1051
DB 683 TCTTCATGAAGAGTCTTCTGAAAGTTGCAGATGCAGATAAACAGCTTGAGCTAGTGCAT 624
QY 1052 TTTTCATCTCGAGCTCTGCTTGTAGATACCAATGCTCAATATCGCCCTCGCATC 1111
DB 623 TTTTCATCTCGAGCTCTGCTTGTAGATATCAAAATGCTCAATATCGCCCTCGCATC 564
QY 1112 TGGCTGCTGCTGCGGTTTATCTGACAGTGTGCTATCAATCGTTGCCAGCACTGGACAA 1171
DB 563 TGGCTGCTGCTGCGGTTTATCTGACAAATGCTATTAATCGTTGCCCTCACTGGACAA 504
QY 1172 AGGCTGCGAGTCTCATAGCAGATACACTAGGACCAACTCTGAGTGCTCGAGATGA 1231
DB 503 AGGTTGGAGTGCATACAGATACACTAGCGACCAACTCTGAGTGTCTCGAGATGA 444
QY 1232 TGGTAGATTTTCCACAGAGGCTGGAACAGTCAAGCTCACTGGGCTGCACAGGAAGTACA 1291
DB 443 TGGTAGATTTTCCACAGAGGCTGGAACAGTCAAGCTCACTGGGCTGCACAGGAAGTACA 384
QY 1292 GTACCTACAGTTTCGGTGGCGGCAAGATTTTGCCTGCGAGATTTCTGCTGAGTGG 1351
DB 383 GTACCTACAGTTTCGGTGGCGGCAAGATTTTGCCTGCGAGATTTCTGCTGAGTGG 324
QY 1352 GAGGACACCGGCTCTTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTG -G 1409
DB 323 GAGGACACCGGCTCTTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTG 264
QY 1410 ATTTTAAAGTTTAAAGTACTCCATGAACAGATGCAGAAACATCGTGTGATGTT 1469
DB 263 GATTTTAAAGTTTAAAGTACTCCGTTGAACAGATGCAGAAACATCGTGTGATGTT 204
QY 1470 GCCCAAAGTGCATCGAATTTCTTTGGAGAGTTATGATTACAACTTTTTTTTATCTAT 1529
DB 203 GCCCAAAGTGCATCGAATTTCTTTGGAGAGTTATGATTAACTGTTTTTTTTATCTATG 144
QY 1530 GTTGAATGACGAGTGCAGGTGCGTGCACGTTGTGCTTGTGTCAGTTTATCTGCGGTAATA 1589
DB 143 CCTGAATGACGAGTGCAGGTGCGTGCAGGT-----CGTTACTGCGGCTAATA 95
QY 1590 CAAACTGTCAGTT 1603
DB 94 CGAACTGTCCTGTT 81

RESULT 12
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CG453107
LOCUS
DEFINITION
CG453107 778 bp DNA linear GSS 17-SEP-2003
CGVSZ27IV ZM.0.7.1.5_KB Zea mays genomic clone ZMBMa0478F05,
genomic survey sequence.
ACCESSION
CG453107
VERSION
CG453107.1 GI:34838107
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 778)
AUTHORS
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
CONSORTIUM
Consortium for Maize Genomics
PUBLISHED
Unpublished (2002)
JOURNAL
Other_GSSs: OGVGSZ7TH
COMMENT
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES
Location/Qualifiers
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Best Local Similarity 86.4%; Pred. No. 3.1e-63;
Matches 584; Conservative 0; Mismatches 5; Indels 87; Gaps 1;
QY 1033 CAGCTTGAGTAGCGGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAATACCAATGCTG 1092
DB 28 CAGCTTGAGTAGCGGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAATACCAATGCTG 87
QY 1093 AATTATCGGCTTCGCAATCTGGCTGCTGCTGCGGTTTATCTGCAAGTGTGCTATCAAT 1152
DB 88 AATTATCGGCTTCGCAATCTGGCTGCTGCTGCGGTTTATCTGCAAGTGTGCTATCAAT 147
QY 1153 CGTTGCCAGCACTGGACAAAGGCTTGCAGTCTCATAGCAGATACACTAGCAGCAACTC 1212
DB 148 CGTTGCCAGCACTGGACAAAGGCTTGCAGTCTCATAGCAGATACACTAGCAGCAACTC 207
QY 1213 CT----- 1214
DB 208 CTGTAAGTCCATTTCAAGTCAGTCTCTCACTGATTAAGTATCTTTATGCTGACTTT 267
QY 1215 -----GGAGTCTCGAGGATCATGTTAGATTTTCAC 1245
DB 268 CTGTGTGTACCTTTTGCTTCTCACCAGGAGTGTCTCGAGGATGATGTTAGATTTTCAC 327
QY 1246 CAGAAGGCTGGAACCAAGTAAAGTCTCACTGCGTGCACAGGAAGTACAGTCTTCAAGTTC 1305
DB 328 CAGAAGGCTGGAACCAAGTAAAGTCTCACTGCGTGCACAGGAAGTACAGTCTTCAAGTTC 387
QY 1306 GGTTCGCTGCCAGATTTTTCGCTGCGAGTTCCTGCTGGAGTCCGGAGGACACGCT 1365
DB 388 GGTTCGCTGCCAGATTTTTCGCTGCGAGTTCCTGCTGGAGTCCGGAGGACACGCT 447
QY 1366 CCTTCAGGTGCAAACTAGTGTGAATCGACCTATTCAACTGGGTGGGATTTTAAAGTTC 1425
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Db      508 AGAATACTCCATGACAAAGATCGAGAAACATCGTGTGATGTTGCTCCCAAAAGTCATCG 567
QY      1486 AATTTCTTTGGAGAGTATGATTAAACAACTTTTTTTTTTTATCTATGTTGAATGACAGTGA 1545
Db      568 AATTTCTTTGGAGAGTATGATTAAACAACTTTTTTTTTTTATCTATGTTGAATGACAGTGA 627
QY      1546 CGGTGCGTCACTGTGTGCTGTGCGAGTTATATCTGCGGCTATATAACAACTGTCCAGTTNT 1605
Db      628 CGGTGCGTCACTGTGTGCTGTGCGAGTTATATCTGCGGCTATATAACAACTGTCCAGTTAT 687
QY      1606 TCTNAAAAAAGAAAAA 1621
Db      688 TCTAAAAAACACAGAA 703

RESULT 13
LOCUS   CG453099/c
DEFINITION
CG453099 779 bp DNA linear GSS 17-SEP-2003
genomic survey sequence.
ACCESSION
CG453099
VERSION
CG453099.1 GI:34838099
KEYWORDS
SOURCE
GSS.
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 779)
REFERENCE
1 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.,
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGVGS27TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 29.7%; Score 485.2; DB 29; Length 779;
Best Local Similarity 86.4%; Pred. No. 3.1e-63;
Matches 584; Conservative 0; Mismatches 5; Indels 87; Gaps 1;
QY 1033 CAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTGGTAGAATACCAAAATGCTG 1092
Db 751 CAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTGGTAGAATACCAAAATGCTG 692
QY 1093 AATTATCGGCTTCGATCGTGGTGTGCTGGGTTTATACGACAGTGTCTATCAAT 1152
Db 691 AATTATCGGCTTCGATCGTGGTGTGCTGGGTTTATACGACAGTGTCTATCAAT 632
QY 1153 CGTTGCCAGCAGTGGCAAAAGGTCTCGAGTCTCATAGCAGATACACTAGCGACCAATC 1212

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Db      631 CGTTGCCAGCAGTGGCAAAAGGTCTCGAGTCTCATAGCAGATACACTAGCGACCAATC 572
QY      1213 CT----- 1214
Db      571 CTGTAAGTCCAAATTCAGTCAAGTTCCTCACTGCAATGATAAGCATCTTTATGCTGACTTT 512
QY      1215 -----GGAGTGTCTCGAGGATGATGCTAGATTTTTCAC 1245
Db      511 CTGTGTACCTTTTGTCTCTCACCAGGAGTGTCTCGAGGATGATGCTAGATTTTTCAC 452
QY      1246 CAGAAGGCTGGAAACCAAGTAAAGTCACTGGCGTGCAAGGAAGTACAGTACCTACAAGTTC 1305
Db      451 CAGAAGGCTGGAAACCAAGTAAAGTCACTGGCGTGCAAGGAAGTACAGTACCTACAAGTTC 392
QY      1306 GGTTCGTGCGCCAAAGATTTTCCCTGCGCAGTTTCTCTGCGAGTGGGAGGACACCGCCT 1365
Db      391 GGTTCGTGCGCCAAAGATTTTCTGCGCAGTTTCTCTGCGAGTGGGAGGACACCGCCT 332
QY      1366 CCTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTGGATTTTAAAGTTTTT 1425
Db      331 CCTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTGGATTTTAAAGTTTTT 272
QY      1426 AGAATCTCATCAACAAGATGCAAGAAACATCGTGTGATGTTGCCCAAAAGTGCATCG 1485
Db      271 AGAATCTCATCAACAAGATGCAAGAAACATCGTGTGATGTTGCCCAAAAGTGCATCG 212
QY      1486 AATTTCTTTGGAGAGTATGATTAAACAACTTTTTTTTTTATCTATGTTGAATGACAGTGA 1545
Db      211 AATTTCTTTGGAGAGTATGATTAAACAACTTTTTTTTTTATCTATGTTGAATGACAGTGA 152
QY      1546 CGGTGCGTCACTGTGTGCTGTGCGAGTTATATCTGCGGCTATATAACAACTGTCCAGTTNT 1605
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QY      1606 TCTNAAAAAAGAAAAA 1621
Db      91 TCTAAAAAACACAGAA 76

RESULT 14
LOCUS   CG278953/c
DEFINITION
CG278953 873 bp DNA linear GSS 25-AUG-2003
genomic survey sequence.
ACCESSION
CG278953
VERSION
CG278953.1 GI:34192236
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 873)
REFERENCE
1 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGV2AT49TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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FEATURES
source

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Db      539 GCTAAGAGTTGTGTAAAGGCTGATTACATGTCCAGTCAACAGATATTAACCTCAAAGATG 598
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